

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 19, 2005, 08:37:45 ; Search time 174 Seconds
(without alignments)
273.697 Million cell updates/sec

Title: us-10-626-530-2

Perfect score: 93

Sequence: 1 MKISVAIPFLITLITLGT.....VCTNPDKWQYIKDKMKN 93

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1512378 seqs, 512079187 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1316

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	93	1	SV14 HUMAN
2	10	10.8	92	2	Q8HYQ3
3	9	9.7	90	1	SV04 CHICK
4	9	9.7	90	2	Q9PW66
5	8	8.6	92	2	Q68A92
6	8	8.6	115	2	Q8HHA0
7	8	8.6	267	2	Q8UF11
8	8	8.6	288	2	Q7CYX2
9	8	8.6	326	2	Q86207
10	8	8.6	818	2	Q7UR95
11	7	7.5	56	2	Q8HYN4
12	7	7.5	67	2	Q9VX52
13	7	7.5	68	2	Q7YX47
14	7	7.5	82	2	Q9BZP4
15	7	7.5	92	1	SV03 HUMAN
16	7	7.5	92	2	Q9MG55
17	7	7.5	93	1	SV03_BOVIN
18	7	7.5	93	2	Q6DUR4
19	7	7.5	115	2	Q66SX0
20	7	7.5	116	2	Q85D00
21	7	7.5	118	2	Q8LX58
22	7	7.5	120	1	SV02_CAVPO
23	7	7.5	162	1	RSD_SALTY
24	7	7.5	162	2	Q8Z327
25	7	7.5	214	2	Q7RU57
26	7	7.5	221	2	Q8EPK2
27	7	7.5	235	1	HXC6_HUMAN
28	7	7.5	235	1	HXC6_MOUSE
29	7	7.5	247	2	Q8TM45
30	7	7.5	255	2	O44332
31	7	7.5	255	2	Q894P3

ALIGNMENTS

32	7	7.5	265	2	Q86727	Q86727 sweet potat
33	7	7.5	289	2	Q8DKJ7	Q8dkj7 synechococ
34	7	7.5	294	2	Q73ZS6	Q73z86 mycobacteri
35	7	7.5	314	2	Q9P3G9	Q9p3g9 neurospora
36	7	7.5	314	2	Q8IY42	Q8iy42 homo sapien
37	7	7.5	314	2	Q9NV03	Q9nv03 homo sapien
38	7	7.5	333	2	Q739T2	Q739t2 bacillus ce
39	7	7.5	335	2	Q81EK1	Q81ek1 bacillus ce
40	7	7.5	337	2	Q7RED0	Q7red0 plasmodium
41	7	7.5	347	2	Q7RNI3	Q7rni3 plasmodium
42	7	7.5	361	2	Q7RM26	Q7rm26 plasmodium
43	7	7.5	363	2	Q9RS42	Q9rs42 deinococcus
44	7	7.5	384	2	Q9LUT0	Q9luc0 arabidopsis
45	7	7.5	381	2	Q755P8	Q755p8 ashbya goss
46	7	7.5	412	2	Q93EX5	Q93ex5 rhodococcus
47	7	7.5	416	2	Q9XE67	Q9xe67 sorghum bic
48	7	7.5	426	2	Q93JT5	Q93jt5 pseudomonas
49	7	7.5	427	2	Q9CNZ7	Q9cnz7 pasteurella
50	7	7.5	427	2	Q9HU16	Q9hu16 pseudomonas
51	7	7.5	427	2	Q9I559	Q9i559 pseudomonas
52	7	7.5	428	2	Q6FTG1	Q6ftg1 candida gla
53	7	7.5	446	2	Q89RE3	Q89r93 bradyrhizob
54	7	7.5	471	2	Q8UHS1	Q8uhs1 agrobacteri
55	7	7.5	474	2	Q8DYR2	Q8dyr2 streptococc
56	7	7.5	474	2	Q8EAB9	Q8eab9 streptococc
57	7	7.5	485	2	Q68X88	Q68x88 rickettsia
58	7	7.5	486	2	Q9ZDP4	Q9zdp4 rickettsia
59	7	7.5	487	2	Q7PBB3	Q7pbb3 rickettsia
60	7	7.5	487	2	Q92IN9	Q92in9 rickettsia
61	7	7.5	494	1	AMYE DROSU	O18420 drosophila
62	7	7.5	499	2	Q9SS65	Q9ss65 arabidopsis
63	7	7.5	540	2	Q94C59	Q94c59 arabidopsis
64	7	7.5	540	2	Q9SA84	Q9sa84 arabidopsis
65	7	7.5	560	2	Q9TB51	Q9tb51 platyneireis
66	7	7.5	575	1	MBHL WOLSU	P31883 wolinnella s
67	7	7.5	584	2	P913I6	P913i6 caenorhabdi
68	7	7.5	616	2	Q8UAV6	Q8uav6 agrobacteri
69	7	7.5	627	2	P74489	P74489 synechocyst
70	7	7.5	797	2	Q16824	Q16824 homo sapien
71	7	7.5	798	2	Q9HAU3	Q9ha43 homo sapien
72	7	7.5	1567	2	Q6MIA1	Q6mia1 bdellovibri
73	7	7.5	1726	2	Q6G4Z9	Q6g4z9 bartonella
74	7	7.5	2850	1	HORN HUMAN	Q86y23 homo sapien
75	6	6.5	43	2	Q13384	Q13384 homo sapien
76	6	6.5	46	2	Q13385	Q13385 homo sapien
77	6	6.5	51	2	Q7RA10	Q7ra10 plasmodium
78	6	6.5	51	2	Q8FE64	Q8fe64 escherichia
79	6	6.5	58	2	Q9TSJ3	Q9tsj3 oryctolagus
80	6	6.5	64	2	Q6H6S2	Q6h6s2 oryza sativ
81	6	6.5	68	2	Q8SXH7	Q8sxh7 drosophila
82	6	6.5	77	2	Q67TC2	Q67tc2 symbiobacte
83	6	6.5	77	2	Q93194	Q93194 african swi
84	6	6.5	77	2	Q9WLW7	Q9wlw7 african swi
85	6	6.5	78	2	Q93190	Q93190 african swi
86	6	6.5	78	2	Q65266	Q65266 african swi
87	6	6.5	78	2	Q9WLW6	Q9wlw6 african swi
88	6	6.5	80	2	Q14745	Q14745 homo sapien
89	6	6.5	80	2	Q6GXJ2	Q6gxj2 gallus gall
90	6	6.5	80	2	Q9DC58	Q9dc58 gallus gall
91	6	6.5	82	1	9KO HUMAN	P13994 homo sapien
92	6	6.5	84	2	Q6U287	Q6u287 homo sapien
93	6	6.5	84	2	Q7KPD3	Q7kpd3 caenorhabdi
94	6	6.5	84	2	Q804P1	Q804p1 pseudopleur
95	6	6.5	85	2	Q9XHJ3	Q9xhj3 arabidopsis
96	6	6.5	87	1	PSK4 ARATH	Q9szq4 arabidopsis
97	6	6.5	87	2	Q7PCB9	Q7pcb9 arabidopsis
98	6	6.5	89	2	Q8C2W1	Q8c2w1 mus muscu
99	6	6.5	91	2	Q49892	Q49892 mycobacteri
100	6	6.5	92	1	SV04_MOUSE	P14097 mus musculu

RESULT 1
SY14 HUMAN
ID SY14 HUMAN STANDARD; PRT; 93 AA.
AC Q16627; Q13954;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A14 precursor (CCL14) (Chemokine CC-1(CC-3)
DE (HCC-1/HCC-3) (HCC-1(1-74)) (NCC-2) [Contains: HCC-1(3-74); HCC-1(4-
DE 74); HCC-1(9-74)].
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 20-93.
RC TISSUE=Bone marrow;
RX MEDLINE=96136773; PubMed=8551235;
RA Schulz-Knappe P., Maegert H.-J., Dewald B., Meyer M., Cetin Y.,
RA Kubites M., Tomeczkowski J., Kirchhoff K., Raida M., Adermann K.,
RA Kist A., Reinecke M., Sillard R., Pardigol A., Uguccioni M.,
RA Baggolini M., Forssmann W.-G.;
RT "HCC-1, a novel chemokine from human plasma.";
RL J. Exp. Med. 183:295-299(1996).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98263352; PubMed=9600961; DOI=10.1073/pnas.95.11.6308;
RA Pardigol A., Forssmann U., Zucht H.-D., Loetscher P.,
RA Schulz-Knappe P., Baggolini M., Forssmann W.-G., Maegert H.-J.;
RT "HCC-2, a human chemokine: gene structure, expression pattern, and
RT biological activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:6308-6313(1998).
[3]
RN SEQUENCE FROM N.A.
RX MEDLINE=99228475; PubMed=10213461; DOI=10.1089/10799099314153;
RA Nomiya H., Fukuda S., Iio M., Tanase S., Miura R., Yoshie O.;
RT "Organization of the chemokine gene cluster on human chromosome
RT 17q11.2 containing the genes for CC chemokine MPIF-1, HCC-2, LEC, and
RT RANTES.";
RL J. Interferon Cytokine Res. 19:227-234(1999).
[4]
RN SEQUENCE FROM N.A. (ISOFORM HCC-1).
RC TISSUE=Pancreas, and Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie H.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.W., Green E.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RN SEQUENCE OF 20-32, IDENTIFICATION OF HCC-1(3-74) AND HCC-1(4-74), MASS
RN SPECTROMETRY, AND CARBOHYDRATE-LINKAGE SITE SER-26.
RX PubMed=10978165; DOI=10.1021/bi992488q;
RA Richter R., Schulz-Knappe P., John H., Forssmann W.-G.;
RT "Posttranslationally processed forms of the human chemokine HCC-1.";

Biochemistry 39:10799-10805(2000).
[6]
RN SEQUENCE OF 20-48, IDENTIFICATION OF HCC-1(9-74), MASS SPECTROMETRY,
RN AND FUNCTION.
RX PubMed=11085751;
RA Dethoux M., Staendker L., Vakili J., Muench J., Forssmann U.,
RA Adermann K., Poehlmann S., Vaseart G., Kirchhoff F., Parmentier M.,
RA Forssmann W.-G.;
RT "Natural proteolytic processing of hemofiltrate CC chemokine 1
RT generates a potent CC chemokine receptor (CCR)1 and CCR5 agonist with
RT anti-HIV properties.";
RL J. Exp. Med. 192:1051-1058(2000).
CC -I- FUNCTION: Has weak activities on human monocytes and acts via
CC receptors that also recognize MIP-1 alpha. It induced
CC intracellular Ca(2+) changes and enzyme release, but no
CC chemotaxis, at concentrations of 100-1,000 nM, and was inactive on
CC T lymphocytes, neutrophils, and eosinophil leukocytes. Enhances
CC the proliferation of CD34 myeloid progenitor cells. The processed
CC form HCC-1(9-74) is a chemotactic factor that attracts monocytes
CC eosinophils, and T-cells and is a ligand for CCR1, CCR3 and CCR5.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC Event=Alternative splicing; Named isoforms=2;
CC Name=HCC-1;
CC IsoId=Q16627-1; Sequence=Displayed;
CC Name=HCC-3;
CC IsoId=O16627-2; Sequence=VSP_001060;
CC -I- TISSUE SPECIFICITY: Expressed constitutively in several normal
CC tissues: spleen, liver, skeletal and heart muscle, gut, and bone
CC marrow, present at high concentrations (1-80 nM) in plasma.
CC -I- PTM: The N-terminal processed forms HCC-1(3-74), HCC-1(4-74) and
CC HCC-1(9-74) are produced in small amounts by proteolytic cleavage
CC after secretion in blood.
CC -I- PTM: HCC-1(1-74), but not HCC-1(3-74) and HCC-1(4-74), is
CC partially O-glycosylated; the O-linked glycan consists of one Gal-
CC GalNAc disaccharide, further modified by two N-acetylneuraminic
CC acids.
CC -I- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.

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CC EMBL; Z49270; CAA89264.1; -;
CC EMBL; Z70292; CAA94307.1; -;
CC EMBL; Z70293; CAA94309.1; -;
CC EMBL; Z49269; CAA89263.1; -;
CC EMBL; AF088219; AAC63329.1; -;
CC EMBL; AF088219; AAF23982.1; -;
CC EMBL; BC045165; AAH45165.1; -;
CC HSSP; P13236; 1HUM.
CC Genew; HGNC:10612; CCL14.
CC MIM; 601392; -;
CC GO; GO:0005615; C:extracellular space; TAS.
CC GO; GO:0004871; F:signal transducer activity; TAS.
CC GO; GO:0006874; P:calcium ion homeostasis; TAS.
CC GO; GO:0006284; P:positive regulation of cell proliferation; TAS.
CC InterPro; IPR000827; CC_chemokine_sml.
CC InterPro; IPR001811; Chemokine_IL8.
CC Pfam; PF00048; IL8; 1.
CC PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
CC Alternative splicing; Cytokine; Direct protein sequencing;
KW Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 93 Small inducible cytokine A14.
FT CHAIN 22 93 HCC-1(3-74).
FT CHAIN 23 93 HCC-1(4-74).
FT CHAIN 28 93 HCC-1(9-74).
FT DISULFID 35 59 By similarity.

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FT DISULFID 36 75 By similarity.
FT CARBOHYD 26 26 O -> OTGGKPKVVKIQLKLG (in isoform HCC-
FT VARSPLIC 27 27 3).
FT FT
FT SEQUENCE 93 AA; 10678 MW; DDB899DC9148836 CRC64;
Query Match 100.0%; Score 93; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 4.9e-94;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKISVAIPPELLITIALGTETSSSRGPHSPSCCTTYTYKIPRIMDYETNSQCS 60
Db 1 MKISVAIPPELLITIALGTETSSSRGPHSPSCCTTYTYKIPRIMDYETNSQCS 60
Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93
Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93
RESULT 2
Q8HYQ3 PRELIMINARY; PRT; 92 AA.
AC Q8HYQ3
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chemokine CCL3/MP-1ALPHA.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22123042; PubMed=12126650; DOI=10.1006/cyto.2002.0875;
RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
RT "Molecular cloning and sequencing of 25 different rhesus macaque
RT chemokine cDNAs reveals evolutionary conservation among C, CC, CX,
RT AND CX3C families of chemokines.";
RL Cytokine 18:140-148(2002)
DR EMBL; AF492866; AAN76070.1; -.
DR HSP; P10147; I850.
DR GO; GO:000576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 92 AA; 10120 MW; 021CAA371143D12A CRC64;
Query Match 10.8%; Score 10; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 54 ETNSQCSKPG 63
Db 52 ETNSQCSKPG 61
RESULT 3
SY04_CHICK STANDARD; PRT; 90 AA.
AC Q90826; Q910C9;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A4 homolog precursor (Macrophage inflammatory
DE protein 1-beta homolog).
GN Name=CCL4; Synonyms=SCYA4;
OS Gallus gallus (Chicken).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95369710; PubMed=7642115; DOI=10.1016/0378-1119(95)00210-W;
RA Petrenko O., Ischenko I., Enrietto P.J.;
RT "Isolation of a cDNA encoding a novel chicken chemokine homologous to
RT mammalian macrophage inflammatory protein-1 beta.";
RL Gene 160:305-306(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20049023; PubMed=10582310;
RA Hughes S., Bumstead N.;
RT "Mapping of the gene encoding a chicken homologue of the mammalian
RT chemokine SCYA4.";
RL Anim. Genet. 30:404-404(1999).
RN [3]
RP SEQUENCE OF 14-90 FROM N.A.
RA Petrenko O., Enrietto P.J.;
RT Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Monokine with inflammatory and chemokinetic properties
CC (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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CC
CC EMBL; L34553; AAA48747.1; -.
CC EMBL; AJ243034; CAB45103.1; -.
CC HSP; P13236; IHUM.
CC InterPro; IPR000827; CC_chemkine_sml.
CC InterPro; IPR001811; Chemokine_IL8.
CC Pfam; PF00048; IL8; 1.
CC PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
CC Chemotaxis; Cytokine; Signal.
KW CHAIN 1 21 By similarity.
FT DISULFID 22 90 Small inducible cytokine A4 homolog.
FT DISULFID 32 56 By similarity.
FT DISULFID 33 72 By similarity.
FT CONFLICT 87 87 M -> L (in Ref. 1).
SQ SEQUENCE 90 AA; 9987 MW; 50AF9679A267408F CRC64;
Query Match 9.7%; Score 9; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 51 DYETNSQC 59
Db 48 DYETNSQC 56
RESULT 4
Q9PWA6 PRELIMINARY; PRT; 90 AA.
AC Q9PWA6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Chemokine.
GN Name=SCYA4;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
```

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OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Hughes S.M., Bumstead N.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF146730; AAD48772.1; -.
DR HSSP; P13236; 1HUM.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; P:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR PFAM; PF00048; IL8; 1.
DR SMART; SM001199; SCV; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 90 AA; 9986 MW; 50AF9679A26751CB CRC64;

Query Match 9.7%; Score 9; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 DYETNSQC 59
Db |||||
48 DYETNSQC 56

RESULT 5
Q68A92
ID Q68A92 PRELIMINARY; PRT; 92 AA.
AC Q68A92;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CC chemokine ligand 3.
GN Names=CC3;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Tsukui T., Sakaguchi M., Maeda S., Koyanagi M., Masuda K., Ohno K.,
RA Tsujimoto H., Iwabuchi S.;
RT "Expression analysis of gene in canine atopic dermatitis.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB164618; BAD42447.1; -.
DR InterPro; IPR001811; Chemokine_IL8.
DR PFAM; PF00048; IL8; 1.
DR SMART; SM001199; SCV; 1.
SQ SEQUENCE 92 AA; 10029 MW; 9D44596B37FD6910 CRC64;

Query Match 8.6%; Score 8; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 SQCSKPCI 64
Db |||||
55 SQCSKPCI 62

RESULT 6
Q8HHA0
ID Q8HHA0 PRELIMINARY; PRT; 115 AA.
AC Q8HHA0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADH subunit 3.
OS Cynocephalus variegatus (Flying lemur).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Dermoptera; Cynocephalidae; Cynocephalus.

OX NCBI_TaxID=9457;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22337212; PubMed=12446821;
RA Schmitz J., Ohme M., Suryobroto B., Zischler H.;
RT "The colugo (Cynocephalus variegatus, Dermoptera): the primates'
RT gliding sister?";
RL Mol. Biol. Evol. 19:2308-2312(2002).
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- SIMILARITY: Belongs to the complex I subunit 3 family.
DR EMBL; AF460846; AAN84904.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR InterPro; IPR000440; Oxidored_q4.
DR PFAM; PF00507; Oxidored_q4; 1.
DR KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SQ SEQUENCE 115 AA; 13041 MW; DE6CDE362DD15DA5 CRC64;

Query Match 8.6%; Score 8; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FLLITIAL 18
Db |||||
15 FLLITIAL 22

RESULT 7
Q8UF11
ID Q8UF11 PRELIMINARY; PRT; 267 AA.
AC Q8UF11;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein Atul591.
GN OrderedCusNames=Atul591;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dupont;
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323(2001).
DR EMBL; AB009116; AAL42593.1; -.
DR PIR; AC2772; AC2772.
DR PIR; B97552; B97552.
DR PFAM; PF01925; DUF81; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 267 AA; 28091 MW; CCDF37F1F6C84F6C CRC64;

Query Match 8.6%; Score 8; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FLLITIAL 18
Db |||||
109 FLLITIAL 116

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RESULT 8
Q7CYX2 PRELIMINARY; PRT; 288 AA.
AC Q7CYX2
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE AGR C 2926p.
GN OrderedLocNames=AGR C 2926;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cereon;
RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Akenazi M., Halling C., Mullin L.,
RA Houmieu K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Planagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
DR EMBL; AE008081; AAK87371.1; -.
DR InterPro; IPR002781; DUF81.
DR Pfam; PF01925; DUF81; 1.
SQ SEQUENCE 288 AA; 30488 MW; 25BB853798BD147D7 CRC64;

Query Match 8.6%; Score 8; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 FLLITIAL 18
Db 130 FLLITIAL 137

RESULT 9
Q86207 PRELIMINARY; PRT; 326 AA.
AC Q86207
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE VP7.
OS Human rotavirus II type 1.
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus; Human rotavirus A;
OC Human rotavirus 2.
OX NCBI_TaxID=36432;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K8;
RX MEDLINE=89342660; PubMed=2474677;
RA Taniguchi K., Nishikawa K., Urasawa T., Urasawa S., Midthun K.,
RA Kapikian A.Z., Gorziglia M.;
RT "Complete nucleotide sequence of the gene encoding VP4 of a human
RT rotavirus (strain K8) which has unique VP4 neutralization epitopes."
RL J. Virol. 63:4101-4106(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K8;
RA Taniguchi K.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; D16344; BAA03848.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR InterPro; IPR001963; VP7.
DR Pfam; PF00434; VP7; 1.
DR ProDom; PD000191; VP7; 1.
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SQ SEQUENCE 326 AA; 37371 MW; 998F71C5D8722C87 CRC64;

Query Match 8.6%; Score 8; DB 2; Length 326;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 FLLITIAL 18
Db 37 FLLITIAL 44

RESULT 10
Q7UR95 PRELIMINARY; PRT; 818 AA.
AC Q7UR95
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Polyrribonucleotide nucleotidyltransferase (EC 2.7.7.8).
GN Name=ppp; OrderedLocNames=RB5804;
OS Rhodopirella baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1."
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294143; CA074445.1; -.
DR HSP; Q53597; IE3P.
DR GO; GO:0000175; F:3'-5'-exoribonuclease activity; IEA.
DR GO; GO:0004654; F:polyribonucleotide nucleotidyltransferase a. . .; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006396; P:RNA processing; IEA.
DR InterPro; IPR001247; 3 Exonase.
DR InterPro; IPR004087; KH.
DR InterPro; IPR004088; KH_type_1.
DR InterPro; IPR003029; S1.
DR Pfam; PF00013; KH 1; 1.
DR Pfam; PF03726; PNase 1.
DR Pfam; PF01138; RNase PH; 2.
DR Pfam; PF03725; RNase PH_C; 2.
DR Pfam; PF00575; S1; 1.
DR SMART; SM00322; KH; 1.
DR SMART; SM00316; S1; 1.
DR PROSITE; PS50084; KH_TYPE_1; 1.
DR PROSITE; PS50126; S1; 1.
KW Complete proteome; Nucleotidyltransferase; Transferase.
SQ SEQUENCE 818 AA; 88221 MW; 1A57F962C413B17A CRC64;

Query Match 8.6%; Score 8; DB 2; Length 818;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 LITIALGT 20
Db 417 LITIALGT 424

RESULT 11
Q8HYN4 PRELIMINARY; PRT; 56 AA.
AC Q8HYN4
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
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DE Macrophage inflammatory protein 1 alpha (Fragment).
OS *Macaca mulatta* (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22074459; PubMed=12079558; DOI=10.1089/08922202760019329;
RA Hofmann-Lehmann R., Williams A.L., Swenerton R.K., Li P.-L.,
RA Rasmussen R.A., Chenine A.-L., McClure H.W., Ruprecht R.M.;
RT "Quantitation of simian cytokine and beta-chemokine mRNAs, using real-
RT time reverse transcriptase-polymerase chain reaction: variations in
RT expression during chronic primate lentivirus infection.";
RL AIDS Res Hum Retroviruses 18:627-639(2002).
DR EMBL; AF457195; AAN76985.1; -.
DR HSSP; P10147; IB50.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; P:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_I18.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
FT NON_TER 1 56
FT TER 56
SQ SEQUENCE 56 AA; 6442 MW; EB12A0E0D41D5F68 CRC64;
Query Match 7.5%; Score 7; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 57 SQCSKPG 63
Db 26 SQCSKPG 32
RESULT 12
Q9VX52 PRELIMINARY; PRT; 67 AA.
AC Q9VX52;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE G12994-PA.
GN ORFNames=CG12994;
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10711132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abail J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke S., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
RT *melanogaster* euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.B., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AS003505; AAF48728.1; -.
DR IntAct; Q9VX52; -.
DR FlyBase; Fgn0040877; CGI2994;
SQ SEQUENCE 67 AA; 7578 MW; 27EDCC7A294303BE CRC64;
Query Match 7.5%; Score 7; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 LLITIAL 18
|||||

Db 42 LLITIAL 48

RESULT 13

Q7YX47

ID Q7YX47 PRELIMINARY; PRT; 68 AA.

AC Q7YX47

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Hypothetical protein C38C10.6.

GN ORENAMES=C38C10.6;

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RN SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RK MEDLINE=99069613; PubMed=9851916;

RA none;

RA "Genome sequence of the nematode C.elegans: A platform for

RT investigating biology.";

RL Science 282:2012-2018(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Thomas K.;

RL Submitted (DSC-1992) to the EMBL/GenBank/DBJ databases.

DR EMBL: Z19153; CAE17766.1; -.

DR WormBase; WBGene00008002; C38C10.6.

DR WormPep; C38C10.6; CE34740.

KW Hypothetical protein.

SQ SEQUENCE 68 AA; 7893 MW; 5DF6271284D43973 CRC64;

Query Match 7.5%; Score 7; DB 2; Length 68;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LLITIAL 18

Db 12 LLITIAL 18

RESULT 14

Q9B2P4

ID Q9B2P4 PRELIMINARY; PRT; 82 AA.

AC Q9B2P4

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Putative C18orf2 variant 1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RN SEQUENCE FROM N.A.

RC TISSUE=Retina;

RK MEDLINE=21098486; PubMed=11173868;

RA Stohr H., Mah N., Schulz H.L., Gehrig A., Frohlich S., Weber B.H.;

RT "EST mining of the Unigene dataset to identify retina-specific

RT genes.";

RL Cytogenet. Cell Genet. 91:267-277(2000).

RN [2]

RN SEQUENCE FROM N.A.

RC TISSUE=Retina;

RA Stohr H., Schulz H.L., Mah N., Gehrig A., Froehlich S., Weber B.H.F.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF295726; AAK13319.1; -.

SQ SEQUENCE 82 AA; 9406 MW; 5162CA14CED467B5 CRC64;

Query Match 7.5%; Score 7; DB 2; Length 82;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LLITIAL 18

Db 21 LLITIAL 27

RESULT 15

SY03 HUMAN

ID SY03 HUMAN STANDARD; PRT; 92 AA.

AC P10147;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Small inducible cytokine A3 precursor (CC13)

DE protein 1-alpha (MIP-1-alpha) (Tonsillar lymphocyte LD78 alpha

DE protein) (G0/G1 switch regulatory protein 19-1) (GOS19-1 protein)

DE (SIS-beta) (PAT 464.1) [Contains: MIP-1-alpha(4-69) (LD78-alpha(4-

DE 69))].

GN Names=CC13; Synonyms=GOS19-1, MIP1A, SCYA3;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=86223879; PubMed=3086300;

RA Obaru K., Fukuda M., Maeda S., Shimada K.;

RT "A cDNA clone used to study mRNA inducible in human tonsillar

RT lymphocytes by a tumor promoter.";

RL J. Biochem. 99:885-894(1986).

RN [2]

RN SEQUENCE FROM N.A.

RP MEDLINE=89140347; PubMed=2521882;

RA Zipfel P.F., Balke J., Irving S.G., Kelly K., Siebenlist U.;

RT "Mitogenic activation of human T cells induces two closely related

RT genes which share structural similarities with a new family of

RT secreted factors.";

RL J. Immunol. 142:1582-1590(1989).

RN [3]

RN SEQUENCE FROM N.A.

RP MEDLINE=91103879; PubMed=22711120;

RA Blum S., Forsdyke R.E., Forsdyke D.R.;

RT "Three human homologs of a murine gene encoding an inhibitor of stem

RT cell proliferation.";

RL DNA Cell Biol. 9:589-602(1990).

RN [4]

RN SEQUENCE FROM N.A.

RP MEDLINE=90287155; PubMed=1694014;

RA Nakao M., Nomiyama H., Shimada K.;

RT "Structures of human genes coding for cytokine LD78 and their

RT expression.";

RL Mol. Cell. Biol. 10:3646-3658(1990).

RN [5]

RN SEQUENCE OF 23-92 FROM N.A.

RA Jang J.S., Kim B.E.;

RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

RN [6]

RN SEQUENCE OF 24-92, AND MUTAGENESIS OF ASP-49.

RK MEDLINE=96127782; PubMed=8541527;

RA Hunter M.G., Bawden L., Brotherton D., Craig S., Cribbes S.,

RA Czaplewski L.G., Dexter T.M., Drummond A.H., Gearing A.H.,

RA Heyworth C.M., Lord B.I., Mccourt M., Varley P.G., Wood L.M.,

RA Edwards R.M., Lewis P.J.;

RT "BB-10010: an active variant of human macrophage inflammatory protein-

RT 1 alpha with improved pharmaceutical properties.";

RL Blood 86:4400-4408(1995).

RN [7]

RN SEQUENCE OF 27-40 AND 71-83, AND FUNCTION.

RK MEDLINE=96106406; PubMed=8525373;

RA Cocchi F., Devico A.J., Garzino-Demo A., Arya S.K., Gallo R.C.,

RA Lusso P.;

RT "Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major
RT HIV-suppressive factors produced by CD8+ T cells.";
RL Science 270:1811-1815(1995).
RN [8]
RP SEQUENCE OF 27-51, AND IDENTIFICATION OF LD78-ALPHA(4-69).
RX PubMed=7537510;
RA Boratini R., Lugini W., Sorzani S., Bottazzi B., Ruggiero P.,
RA Borsachi D., Saggioro D., Chicco-Blanchi L., Proost P., van Damme J.,
RA Mantovani A.;
RT "Identification of MIP-1 alpha/LD78 as a monocyte chemoattractant
RT released by the HTLV-1-transformed cell line MT4.";
RL AIDS Res. Hum. Retroviruses 11:155-160(1995).
RN [9]
RP SUBUNIT, AND INTERACTION WITH MIP-1-BETA(3-69).
RX PubMed=12070155; DOI=10.1074/jbc.M203077200;
RA Guan E., Wang J., Rodriguez G., Norcross M.A.; /CCL4 affects receptor
RT "Natural truncation of the chemokine MIP-1beta /CCL4 affects receptor
RT specificity but not anti-HIV-1 activity.";
RL J. Biol. Chem. 277:32348-32352(2002).
RN [10]
RP REVIEW
RX PubMed=12401480; DOI=10.1016/S1359-6101(02)00045-X;
RA Menten P., Wuyts A., Van Damme J.;
RT "Macrophage inflammatory protein-1.";
RL Cytokine Growth Factor Rev. 13:455-481(2002).
RN [11]
RP STRUCTURE OF 24-92 BY NMR, AND MUTAGENESIS OF ASP-49 AND GLU-89.
RX PubMed=10347159; DOI=10.1074/jbc.274.23.18077;
RA Czaplewski L.G., McKeating J., Craven C.J., Higgins L.D., Appay V.,
RA Brown A., Dudgeon T., Howard L.A., Meyers T., Owen J., Palan S.R.,
RA Tan P., Wilson G., Woods N.R., Heyworth C.M., Lord B.I.,
RA Brotherton D., Christison R., Craig S., Cribbes S., Edwards R.M.,
RA Evans S.J., Gilbert R., Morgan P., Elliot Randle E., Schofield N.,
RA Varley P.G., Fisher J., Jonathan P., Waltho J.P., Hunter M.G.;
RT "Identification of amino acid residues critical for aggregation of
RT human CC chemokines macrophage inflammatory protein (MIP)-1alpha, MIP-
RT 1beta, and RANTES. Characterization of active disaggregated chemokine
RT variants.";
RL J. Biol. Chem. 274:16077-16084(1999).
CC -1- FUNCTION: Monokine with inflammatory and chemokinetic properties.
CC Binds to CCR1, CCR4 and CCR5. One of the major HIV-suppressive
CC factors produced by CD8+ T cells. Recombinant MIP-1-alpha induces
CC a dose-dependent inhibition of different strains of HIV-1, HIV-2,
CC and simian immunodeficiency virus (SIV).
CC -1- SUBUNIT: Self-associates. Also heterodimer of MIP-1-alpha(4-69)
CC and MIP-1-beta(3-69).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- INDUCTION: By TPA or PHA (TPA = 12-o-tetradecanoyl phorbol-13
CC acetate (tumor promoter); PHA = phytohemagglutinin (T-cell
CC mitogen)).
CC -1- PTM: N-terminal processed form LD78-alpha(4-69) is produced by
CC proteolytic cleavage after secretion from HTLV1-transformed T-
CC cells.
CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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CC
CC ENBL; D00044; BAA00029.1; -;
CC ENBL; M23452; AAA36316.1; -;
CC ENBL; M25315; AAA57255.1; -;
CC ENBL; X03754; CAA27388.1; -;
CC ENBL; X04018; CAA27643.1; ALT_SEQ.
CC ENBL; M23178; AAA35858.1; -;
CC ENBL; D90144; BAA14172.1; -;
CC ENBL; AF043339; AAC03539.1; -;
CC PIR; A35673; A30574.
CC PDB; 1B50; NMR; A/B=24-92.

DR PDB; 1B53; NMR; A/B=24-92.
DR Genew; HGNC:10627; CCL3.
DR MIM; 182283; -;
DR GO; GO:0005625; -; C:soluble fraction; TAS.
DR GO; GO:0008009; F:chemokine activity; TAS.
DR GO; GO:0004871; F:signal transducer activity; TAS.
DR GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . .; TAS.
DR GO; GO:0006874; P:calcium ion homeostasis; TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; TAS.
DR GO; GO:0006887; P:exocytosis; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR GO; GO:0045069; P:regulation of viral genome replication; TAS.
DR GO; GO:0007185; P:signal transduction; TAS.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW 3D-structure; Chemotaxis; Cytokine; Direct protein sequencing;
KW Inflammatory response; Signal.
FT SIGNAL 1 23
FT CHAIN 24 92 Small inducible cytokine A3.
FT CHAIN 27 92 MIP-1-alpha(4-69).
FT DISULFID 33 57 By similarity.
FT DISULFID 34 73 By similarity.
FT MUTAGEN 49 49 D->A: Reduces self-association; in BB-
FT 10010: Improved pharmaceutical
FT properties.
FT E->A: Reduces self-association.
FT MUTAGEN 89 89
FT TURN 44 46
FT STRAND 49 51
FT TURN 55 58
FT STRAND 63 65
FT TURN 67 68
FT TURN 76 77
FT HELIX 79 84
FT TURN 85 88
FT SEQUENCE 92 AA; 10085 MW; 517865D5D6776CA8 CRC64;
SQ
Query Match 7.5%; Score 7; DB 1; Length 92;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 57 SQCSKPG 63
Db 55 SQCSKPG 61
RESULT 16
Q9MG95 PRELIMINARY; PRT; 92 AA.
AC Q9MG95;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein S19.
GN Names=rp19;
OS Chrysodidymus synuroides.
OC Mitochondrion.
OC Eukaryota; stramenopiles; Chrysophyceae; Synurales; Chrysodidymus.
OX NCBI_TaxID=47573;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20330374; PubMed=10871400; DOI=10.1093/nar/28.13.2512;
RA Chesnick J.M., Goff M., Graham J., Ocampo C., Lang B.F., Seif E.,
RA Burger G.;
RT "The mitochondrial genome of the stramenopile alga Chrysodidymus
RT synuroides. Complete sequence, gene content and genome
RT organization.";
RL Nucleic Acids Res. 28:2512-2518(2000).


```

CC -!- SIMILARITY: Belongs to the S19P family of ribosomal proteins.
DR EMBL; AF222716; AAF36954.1; -.
DR HSP; P80381; IQPF.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR002222; Ribosomal_S19.
DR Pfam; PF00203; Ribosomal_S19; 1.
DR PRINTS; PR00975; RIBOSOMALS19.
DR PRODOM; PD01012; Ribosomal_S19; 1.
DR PROSITE; PS00323; RIBOSOMAL_S19; 1.
KW Mitochondrion; Ribonucleoprotein; Ribosomal protein.
SQ SEQUENCE 92 AA; 11031 MW; 4DDA141178B58C74 CRC64;

Query Match 7.5%; Score 7; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AIPFLL 13
DB 34 AIPFLL 40

RESULT 17
SY03_BOVIN STANDARD; PRT; 93 AA.
AC Q89QA6;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory
protein 1-alpha) (MIP-1-alpha).
GN Name=CCL3; Synonyms=SCYA3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
RP SEQUENCE FROM N.A.
RA Werling D.;
RT "Role of chemokines in RSV infection.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Monokine with inflammatory and chemokinetic properties.
CC Binds to CCR1, CCR4 and CCR5 (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.

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DR EMBL; AY077840; AAL78060.1; -.
DR InterPro; IPR000827; CC_chemokine.sml.
DR PRINTS; PR00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Inflammatory response; Signal.
FT SIGNAL 1 24 By similarity.
FT CHAIN 25 93 Small inducible cytokine A3.
FT DISULFID 34 58 By similarity.
FT DISULFID 35 74 By similarity.
SQ SEQUENCE 93 AA; 10118 MW; 1266BFBFCBE58E9 CRC64;

Query Match 7.5%; Score 7; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 57 SQCSKPG 63
DB 56 SQCSKPG 62

RESULT 18
Q6DUK4
AC Q6DUK4 PRELIMINARY; PRT; 93 AA.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Macrophage inflammatory protein 1 alpha.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
[1]
RP SEQUENCE FROM N.A.
RA Stirling C.M.A.; Takamatsu H.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY643423; AAT65077.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 93 AA; 10117 MW; 0B8D26CABE28414C CRC64;

Query Match 7.5%; Score 7; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 SQCSKPG 63
DB 56 SQCSKPG 62

RESULT 19
Q6ESX0
AC Q6ESX0 PRELIMINARY; PRT; 115 AA.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE NADH dehydrogenase subunit 3.
GN Name=nad3;
OS Diplometopon zarudnyi (Zarudnyi's worm lizard).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Amphisbaenia; Trogonophidae;
OC Diplometopon.
OX NCBI_TaxID=94420;
[1]
RP SEQUENCE FROM N.A.
RX PubMed=15324836; DOI=10.1016/j.ympev.2004.05.003;
RA Macey J.R.; Papenfuss T.J.; Kuehl J.V.; Fourcade H.M.; Boore J.L.;
RT "Phylogenetic relationships among amphisbaenian reptiles based on
complete mitochondrial genomic sequences.";
RL Mol. Phylogenet. Evol. 33:22-31(2004).
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- SIMILARITY: Belongs to the complex I subunit 3 family.
DR EMBL; AY605474; AAT08510.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR InterPro; IPR000440; Oxidored g4.
DR Pfam; PF00507; Oxidored g4; 1.
DR Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
KW SEQUENCE 115 AA; 13186 MW; 088A852664ABFE01 CRC64;

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Query Match          7.5%; Score 7; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LLITIAL 18
DB 11 LLITIAL 17

RESULT 20
Q85D00 PRELIMINARY; PRT; 116 AA.
AC Q85D00;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADH dehydrogenase subunit 3.
GN Name=ND3;
OS Platyroctes apus (legless searid).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Argentiniformes; Platyroctidae; Platyroctes.
OX NCBI_TaxID=170202;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22628593; PubMed=12742752; DOI=10.1016/S1055-7903(02)00418-9;
RA Ishiguro N.B., Miya M., Nishida M.;
RT "Basal euteleostean relationships: a mitogenomic perspective on the
RT phylogenetic reality of the "protacanthopterygii";
RL Mol. Phylogenet. Evol. 27:476-488(2003).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SIMILARITY: Belongs to the complex I subunit 3 family.
DR ENBL; AP004107; BAC58219.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR InterPro; IPR000440; Oxidored_q4.
DR Pfam; PF00507; Oxidored_q4; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SQ SEQUENCE 116 AA; 12920 MW; 63250CB6F2B6F276 CRC64;

Query Match          7.5%; Score 7; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LLITIAL 18
DB 8 LLITIAL 14

RESULT 21
Q8LX58 PRELIMINARY; PRT; 118 AA.
AC Q8LX58;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NADH3 protein.
GN Name=nadh3;
OS Cynocephalus variegatus (Flying lemur).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Dermoptera; Cynocephalidae; Cynocephalus.
OX NCBI_TaxID=9457;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22056029; PubMed=12034869; DOI=10.1073/pnas.102164299;
RA Arnason U., Adegoke J.A., Bodin K., Born E.W., Esa Y.B., Gullberg A.,
RA Nilsson M., Short R.V., Xu X., Janke A.;
RT "Mammalian mitogenomic relationships and the root of the eutherian
RT tree.";

Proc. Natl. Acad. Sci. U.S.A. 99:8151-8156(2002).
-1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SIMILARITY: Belongs to the complex I subunit 3 family.
DR ENBL; AJ428849; CAD21800.2; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR InterPro; IPR000440; Oxidored_q4.
DR Pfam; PF00507; Oxidored_q4; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SQ SEQUENCE 118 AA; 13382 MW; F6FE57203218C19 CRC64;

Query Match          7.5%; Score 7; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LLITIAL 18
DB 16 LLITIAL 22

RESULT 22
SY02_CAVPO STANDARD; PRT; 120 AA.
AC Q08782;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A2 precursor (CCf2) (Monocyte chemotactic
DE protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
GN Name=CCf2; Synonyms=MCPI, SCYA2;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Z; TISSUE=Spleen;
RX MEDLINE=93267104; PubMed=8496603;
RA Yoshimura T.;
RT "cDNA cloning of guinea pig monocyte chemoattractant protein-1 and
RT expression of the recombinant protein.";
RL J. Immunol. 150:5025-5032(1993).
CC -1- FUNCTION: Chemotactic factor that attracts monocytes, but not
CC neutrophils.
CC -1- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
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DR ENBL; L04985; AAA37047.1; -.
DR FIR; I48147; I48147.
DR HSSP; P80099; 1B00.
DR InterPro; IPR000827; CC_chemokine_sm1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;
KW Pyrilidone carboxylic acid; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 120 Small inducible cytokine A2.
FT MOD_RES 24 24 Pyrilidone carboxylic acid (By
FT DISULFID 33 57 By similarity.

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FT DISULFID 34 73 BY similarity.
ET CARBOHYD 97 97 N-linked (GLCNAC... ) (Potential).
SQ SEQUENCE 120 AA; 13741 MW; 5905596851CF1C54 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 27; Length 120;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 KWQDYI 87
Db 79 KWQDYI 85

RESULT 23
RSD_SALTY STANDARD; PRT; 162 AA.
AC Q9L9I6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Regulator of sigma D.
GN Name=rsd; OrderedLocusNames=STM4165; ORFNames=STMF1.32;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E.; Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RA "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
CC -I- FUNCTION: Has binding activity to the major sigma subunit of RNA
CC polymerase. May be involved in replacement of the RNA polymerase
CC sigma subunit from sigma-70 to sigma-S during the transition from
CC exponential growth to the stationary phase (By similarity).
CC -I- SIMILARITY: Belongs to the rsd/algQ family.
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DR EMBL; AF170176; AAF33507.1; -
DR EMBL; AE008894; AAL22993.1; -
DR PDB; 1LJA; Model; A=3-155.
DR StyGene; SG7777; red.
DR InterPro; IPR007448; Rsd AlgQ.
DR Pfam; PF04353; Rsd AlgQ; 1.
KW 3D-structure; Complete proteome; Transcription regulation.
SQ SEQUENCE 162 AA; 18653 MW; 60A52C4DB80142D8 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 34; Length 162;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 47 QRIMDYI 53
Db 101 QRIMDYI 107

RESULT 24
Q82327 PRELIMINARY; PRT; 162 AA.
ID Q82327
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AC Q8Z327; Q7C6P6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative regulatory protein.
GN Name=rsd; OrderedLocusNames=STY3720, t3466;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RA "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TY2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodyazani V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL Bacteriol. 185:2330-2337(2003).
DR EMBL; AL627279; CAD09479.1; -
DR EMBL; AE016845; AA070982.1; -
DR GO; GO:0030528; F:transcription regulator activity; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR Pfam; PF04353; Rsd AlgQ; 1.
KW Complete proteome.
SQ SEQUENCE 162 AA; 18683 MW; A2CFCFB82A8842C0 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 34; Length 162;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 47 QRIMDYI 53
Db 101 QRIMDYI 107

RESULT 25
Q7RU57 PRELIMINARY; PRT; 214 AA.
AC Q7RU57;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein B12F1.130.
GN Name=NCU03449.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Reiman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M., Schulte U.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.U., Zelter A., Schulte U.,
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RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kanvesselis M., Mauceli E., Bielek C., Rudd S., Frishman D.,
RA Kryzofova S., Rasmussen C., Merzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbola D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 010-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC ENBL; AABX01000737; EAA27499.1; -.
DR InterPro; IPR001254; Peptidase S1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 214 AA; 23078 MW; B3269D4996764AC0 CRC64;

Query Match 7.5%; Score 7; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 TESSRG 28
14 TESSRG 20
|||||
Db 14 TESSRG 20

RESULT 26
ID QBEK2 PRELIMINARY; PRT; 221 AA.
AC QBEK2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE ABC transporter permease.
DE OrderedLocusNames=OB2099;
GN Oceanobacillus iheyensis.
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OC NCBI_TaxID=182710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HTE831;
RX MEDLINE=222020767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
CC -1- FUNCTION: Part of a binding-protein-dependent transport system.
CC Probably responsible for the translocation of the substrate across
CC the membrane (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family.
CC ENBL; AP004600; BAC14055.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006140; 2-Hacid.DH.C.
DR InterPro; IPR000515; BPD_transp_1;
DR Pfam; PF00528; BPD_transp_1;
DR PROSITE; PS00928; ABC_TMI; 1.
DR PROSITE; PS00065; D_2_HYDROXYACID_DH_1; UNKNOWN_1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 221 AA; 23972 MW; 4C0463264425855 CRC64;

Query Match 7.5%; Score 7; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SVAAPF 10
|||||
Db 101 SVAAPF 107

RESULT 27
HXK6_HUMAN STANDARD; PRT; 235 AA.
ID AC P09630;
DT 01-MAR-1989 (Rel. 10, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Homeobox protein Hox-C6 (Hox-3C) (HHO.C8) (CP25).
GN Name=HOXC6; Synonyms=HOX3C;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=87260899; PubMed=2885844;
RA Simeone A., Mavilio F., Acampora D., Giampaolo A., Faiella A.,
RA Zappavigna V., D'Esposito M., Pannese M., Russo G., Boncinelli E.,
RA Peschle C.;
RT "Two human homeobox genes, c1 and c8: structure analysis and
RT expression in embryonic development.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4914-4918(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=88262550; PubMed=2898768;
RA Simeone A., Pannese M., Acampora D., D'Esposito M., Boncinelli E.;
RT "At least three human homeoboxes on chromosome 12 belong to the same
RT transcription unit.";
RL Nucleic Acids Res. 16:5379-5390(1988).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=90215256; PubMed=2576652;
RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,
RA Gaudino G., Stornaiuolo A., Cafiero M., Faiella A., Simeone A.;
RT "Organization of human class I homeobox genes.";
RL Genome 31:745-756(1989).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P09630-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P09630-2; Sequence=VSP_002392;
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -1- SIMILARITY: Contains 1 homeobox domain.
CC -----
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CC -----
DR ENBL; S82986; AAB46892.1; -.
DR ENBL; M16938; AAA36007.1; -.
DR PIR; B28030; WJHU3C.
DR HSSP; P02833; 9ANT.
DR TRANSFAC; T01742; -.
Qy
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DR Genew; HGNC:5128; HOXC6.
DR MM; 142972; -.
DR GO; GO:0003714; F:transcription corepressor activity; TAS.
DR GO; GO:0007275; P:development; TAS.
DR GO; GO:0006357; P:regulation of transcription from Pol II pro. . .; TAS.
DR InterPro; IPR001827; Antennapedia.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD00010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS50071; HOMEBOX 2; 1.
KW Alternative splicing; Developmental protein; DNA-binding; Homeobox;
KW Nuclear protein; Transcription regulation.
FT SITE 122 127 Antp-type hexapeptide.
FT DNA BIND 141 200 Homeobox.
FT DOMAIN 168 171 Poly-Arg.
FT DOMAIN 208 212 Poly-Gly.
FT DOMAIN 221 235 Glu/Lys-rich.
FT VARSPPLIC 1 82 Missing (in isoform 2).
FT CONFLICT 218 218 M -> L (in Ref. 3).
SQ SEQUENCE 235 AA; 26933 MW; BD68870347CB71C0 CRC64;

Query Match 7.5%; Score 7; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 SSSRGYPY 30
Db 64 SSSRGYPY 70

RESULT 28
HCXC6 MOUSE
ID HCXC6 MOUSE STANDARD; PRT; 235 AA.
AC P10629; O61683;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Homeobox protein Hox-C6 (Hox-3.3) (Hox-6.1).
GN Name=Hoxc6; Synonyms=Hox-3.3, Hoxc-6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94131843; PubMed=7905473;
RA Shimeld S.M., Gaunt S.J., Coletta P.L., Geada A.M., Sharpe P.T.;
RT "Spatial localisation of transcripts of the Hox-C6 gene.";
RL J. Anat. 183:515-523 (1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92102952; PubMed=1684715; DOI=10.1016/0925-4773(91)90063-C;
RA Coletta P.L., Shimeld S.M., Chaudhuri C., Mueller U., Clarke J.P.,
RA Sharpe P.T.;
RT "Characterisation of the murine Hox-3.3 gene and its promoter.";
RL Mech. Dev. 35:129-142 (1991).
RN [3]
RP SEQUENCE OF 15-235 FROM N.A.
RC TISSUE=Bone marrow, and Spleen;
RX MEDLINE=88329001; PubMed=2901346;
RA Kongsuwan K., Webb E., Housiaux P., Adams J.M.;
RT "Expression of multiple homeobox genes within diverse mammalian
RL haemopoietic lineages.";
RN EMO J. 7:2131-2138 (1988).
RN [4]
RP SEQUENCE OF 131-235 FROM N.A.

RC TISSUE=Kidney;
RX MEDLINE=88328811; PubMed=2459223;
RA Sharpe P.T., Miller J.R., Evans E.P., Burtenshaw M.D., Gaunt S.J.;
RT "Isolation and expression of a new mouse homeobox gene.";
RL Development 102:397-407 (1988).
RN [5]
RP SEQUENCE OF 133-235 FROM N.A.
RX MEDLINE=89357988; PubMed=2570032;
RA Shughart K., Pravecheva D., Newman M.S., Huihan L.W., Jiang Z.,
RA Ruddie F.H.;
RT "Isolation and regional localization of the murine homeobox-containing
RL gene Hox-3.3 to mouse chromosome region 15S.";
CC Genomics 5:76-83 (1989).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
a developmental regulatory system that provides cells with
specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=PR11;
CC IsoId=P10629-1; Sequence=Displayed;
CC Name=PR1;
CC IsoId=P10629-2; Sequence=VSP_002393;
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -1- SIMILARITY: Contains 1 homeobox domain.
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EMBL; J03074; AAA37832.1; -
EMBL; M35986; AAA37854.1; -
EMBL; X16511; CAA34518.1; -
EMBL; X16510; CAA34517.1; -
EMBL; S74185; AAB20717.1; -
EMBL; X12504; CAA31022.1; -
EMBL; X12504; CAA31023.1; -
EMBL; X16838; CAA34737.1; -
EMBL; A32167; A32167.
PIR; A56568; A56568.
PIR; S00987; WJMSX6.
HSP; P02833; 9ANT.
TRANSFAC; T01743; -.
MGD; MGI:96197; Hoxc6.
InterPro; IPR001827; Antennapedia.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; Homeobox; 1.
PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR00024; HOMEBOX.
ProDom; PD00010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00032; ANTENNAPEDIA; 1.
PROSITE; PS00027; HOMEBOX 1; 1.
PROSITE; PS50071; HOMEBOX 2; 1.
KW Alternative splicing; Developmental protein; DNA-binding; Homeobox;
KW Nuclear protein; Transcription regulation.
FT SITE 122 127 Antp-type hexapeptide.
FT DNA BIND 141 200 Homeobox.
FT DOMAIN 221 235 Glu/Lys-rich.
FT VARSPPLIC 1 82 Missing (in isoform PR1).
FT CONFLICT 15 18 AGGQ -> QQRP (in Ref. 3).
FT CONFLICT 131 131 S -> N (in Ref. 4).
FT CONFLICT 192 192 R -> A (in Ref. 4).
FT CONFLICT 228 229 TE -> OK (in Ref. 1 and 2).
SQ SEQUENCE 235 AA; 26915 MW; BD695C7347CB71C0 CRC64;
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Query Match          7.5%; Score 7; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 SSSRGPy 30
Db 64 SSSRGPy 70

RESULT 29
Q8TM45 Q8TM45 PRELIMINARY; PRT; 247 AA.
AC Q8TM45;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Predicted protein.
GN OrderedLocNames=MA2825;
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayal L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res.12:532-542(2002).
DR EMBL; AE010982; AAM06204.1; -.
KW Complete proteome.
SQ SEQUENCE 247 AA; 28575 MW; 17EFB83302522318 CRC64;

Query Match          7.5%; Score 7; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ITIALGT 20
Db 73 ITIALGT 79

RESULT 30
O44332 O44332 PRELIMINARY; PRT; 255 AA.
AC O44332;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hemocyte protease-3.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Spingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99124363; PubMed=9927173;
RA Jiang H., Wang Y., Kanost M.R.;
RT "Four serine proteinases expressed in Manduca sexta haemocytes.";
RL Insect Mol. Biol. 8:39-53(1999).
CC -|- SIMILARITY: Belongs to peptidase family S1.

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DR EMBL; AF017665; AAB94559.1; -.
DR HSSP; P00760; 3BTH.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPsin.
DR SMART; SM00020; TRYp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 255 AA; 27683 MW; F0609ECD12C5A8D CRC64;

Query Match          7.5%; Score 7; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 LITIALG 19
Db 14 LITIALG 20

Search completed: September 19, 2005, 08:47:20
Job time : 179 secs

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OM protein - protein search, using sw model

Run on: September 19, 2005, 08:47:31 ; Search time 174 Seconds
(without alignments)
273.697 Million cell updates/sec

Title: US-10-626-530-2

Perfect score: 504

Sequence: 1 MKTSVAIRPFLITLITLGT.....VCTNPDKWQDIKDKEN 93

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	504	100.0	93	1	SV14_HUMAN
2	258.5	51.3	93	2	Q6DUF4
3	240.5	47.7	93	1	SV3L_HUMAN
4	239	47.4	92	2	Q8HYQ3
5	238.5	47.3	93	1	SV03_BOVIN
6	237.5	47.1	92	2	Q711P4
7	236	46.8	92	1	SV03_HUMAN
8	235.5	46.7	90	1	SV04_CHICK
9	235.5	46.7	90	2	Q9PWA6
10	234.5	46.5	92	1	SV04_MOUSE
11	230.5	45.7	92	1	SV04_RABIT
12	229.5	45.5	92	1	SV04_RAT
13	229.5	45.5	92	2	Q8HYQ2
14	228.5	45.3	92	2	Q8NHW4
15	225.5	44.7	92	2	Q68A20
16	224.5	44.5	92	1	SV04_HUMAN
17	223.5	44.3	92	2	Q6NSB0
18	223	44.2	92	1	SV03_MOUSE
19	223	44.2	92	1	SV03_RAT
20	222.5	44.1	92	2	Q91ZL0
21	220	43.7	92	2	Q68A92
22	217.5	43.2	85	2	Q80XG5
23	213.5	42.4	80	2	Q14745
24	209	41.5	86	2	Q8HYN4
25	209	41.5	89	2	Q918E0
26	208	41.3	89	1	SV18_HUMAN
27	201.5	40.0	120	1	SV23_HUMAN
28	199	39.5	92	2	Q91ZG5
29	197	39.1	88	2	Q8HYF8
30	194.5	38.6	92	1	SV05_RAT
31	194.5	38.6	92	2	Q6PDI1

32	191	37.9	91	1	SV05_HUMAN
33	189	37.5	91	1	SV05_MOUSE
34	188	37.3	91	1	SV05_HORSE
35	188	37.3	113	1	SV15_HUMAN
36	183	36.3	91	1	SV05_CANFA
37	183	36.3	91	1	SV05_CAVPO
38	183	36.3	91	2	Q8HYQ1
39	182	36.1	92	1	SV05_FELCA
40	181.5	36.0	120	1	SV16_HUMAN
41	180.5	35.8	91	2	Q8QG57
42	180	35.7	116	1	SV06_MOUSE
43	178.5	35.4	115	2	Q68FP3
44	177.5	35.2	98	1	SV13_CANFA
45	176	34.9	49	2	Q8HYN3
46	176	34.9	101	2	Q64IC2
47	175	34.7	91	1	SV05_BOVIN
48	175	34.7	91	1	SV05_SIGHI
49	173.5	34.4	98	1	SV13_HUMAN
50	173.5	34.4	116	2	Q6IVB4
51	171.5	34.0	101	2	Q8JRS7
52	170.5	33.8	119	2	Q8K477
53	168.5	33.4	122	1	SV09_MOUSE
54	166	32.9	94	2	Q64H35
55	163.5	32.4	94	1	SV26_HUMAN
56	163.5	32.4	101	2	Q672Y4
57	163.5	32.4	119	1	SV24_MOUSE
58	162.5	32.2	92	1	REG1_BOVIN
59	162.5	32.2	120	2	Q8HYP4
60	162	32.1	79	2	Q672V7
61	161	31.9	91	2	Q8QG56
62	160	31.7	95	2	Q98158
63	159	31.5	97	1	EOTA_RAT
64	157.5	31.2	120	2	Q8CGM5
65	156	31.0	125	1	SV02_RABIT
66	155	30.8	99	1	SV08_HUMAN
67	153.5	30.5	99	1	SV02_PIG
68	153	30.4	91	2	Q8AV56
69	153	30.4	99	2	Q68AY9
70	152	30.2	99	2	Q8HYQ0
71	152	30.2	99	2	Q8MKC8
72	152	30.2	99	2	Q865F4
73	151	30.0	99	1	SV02_HORSE
74	151	30.0	99	2	Q95N01
75	150.5	29.9	148	1	SV02_MOUSE
76	150	29.8	50	2	Q8HYN5
77	150	29.8	94	1	SV17_HUMAN
78	150	29.8	97	1	EOTA_MOUSE
79	150	29.8	100	1	EOTA_HORSE
80	150	29.8	101	1	SV02_CANFA
81	149	29.6	148	1	SV02_RAT
82	148.5	29.5	99	1	MCPA_BOVIN
83	148	29.4	99	1	SV08_BOVIN
84	147	29.2	91	2	Q8JIM4
85	146	29.0	91	2	Q8JIM5
86	146	29.0	94	1	VM12_HUV8
87	146	29.0	97	1	EOTA_HUMAN
88	146	29.0	99	1	SV07_HUMAN
89	146	29.0	109	2	Q727Q8
90	144.5	28.7	119	1	SV24_HUMAN
91	144	28.6	99	1	SV08_PIG
92	142	28.2	93	2	Q9ERE0
93	142	28.2	97	2	Q8HXZ5
94	141	28.0	93	1	SV22_HUMAN
95	141	28.0	99	2	Q672X6
96	141	28.0	109	2	Q865F3
97	139	27.6	94	2	Q8HYF9
98	139	27.6	99	2	Q8I021
99	138	27.4	131	2	Q9R043
100	137	27.2	74	1	MCPB_BOVIN

ALIGNMENTS

RESULT 1
SY14 HUMAN
ID -SY14 HUMAN STANDARD; PRT; 93 AA.
AC Q16627; Q13954;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A14 precursor (CCL14) (Chemokine CC-1(CC-3)
DE (HCC-1/HCC-3) (HCC-1(1-74)) (NCC-2) [contains: HCC-1(3-74); HCC-1(4-
DE 74); HCC-1(9-74)].
GN Name=CCL14; Synonyms=NCC2, SCYA14;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 20-93.
RC TISSUE=Bone marrow;
RX MEDLINE=96136773; PubMed=8551235;
RA Schulz-Knappe P., Maegert H.-J., Dewald B., Meyer M., Cetin Y.,
RA Kubbes M., Tomeczkowska J., Kirchhoff K., Raida M., Adermann K.,
RA Kist A., Reinecke M., Sillard R., Pardigol A., Ugucioni M.,
RA Baggolini M., Forssmann W.-G.;
RT "HCC-1, a novel chemokine from human plasma.";
RL J. Exp. Med. 183:295-299(1996).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98263352; PubMed=9600961; DOI=10.1073/pnas.95.11.6308;
RA Pardigol A., Forssmann U., Zucht H.-D., Loetscher P.,
RA Schulz-Knappe P., Baggolini M., Forssmann W.-G., Maegert H.-J.;
RT "HCC-2, a human chemokine: gene structure, expression pattern, and
RT biological activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:6308-6313(1998).
[3]
RN SEQUENCE FROM N.A.
RX MEDLINE=99228475; PubMed=10213461; DOI=10.1085/107999099314153;
RA Nomiya H., Fukuda S., Ito M., Tanase S., Miura R., Yoshie O.;
RT "Organization of the chemokine gene cluster on human chromosome
RT 17q11.2 containing the genes for CC chemokine MPIP-1, HCC-2, LEC, and
RT RANTES.";
RL J. Interferon Cytokine Res. 19:227-234(1999).
[4]
RN SEQUENCE FROM N.A. (ISOFORM HCC-1).
RC TISSUE=Pancreas, and Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J.J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra W.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RN SEQUENCE OF 20-32, IDENTIFICATION OF HCC-1(3-74) AND HCC-1(4-74), MASS
RN SPECTROMETRY, AND CARBOHYDRATE-LINKAGE SITE SER-26.
RX PubMed=10978165; DOI=10.1021/bi992488q;
RA Richter R., Schulz-Knappe P., John H., Forssmann W.-G.;
RT "Posttranslationally processed forms of the human chemokine HCC-1.";

Biochemistry 39:10799-10805(2000).
[6]
RN SEQUENCE OF 20-48, IDENTIFICATION OF HCC-1(9-74), MASS SPECTROMETRY,
RN AND FUNCTION.
RX PubMed=11085751;
RA Dethaux M., Staendker L., Vakili J., Muench J., Forssmann U.,
RA Adermann K., Poehlmann S., Vassart G., Kirchhoff F., Parmentier M.,
RA Forssmann W.-G.;
RT "Natural proteolytic processing of hemofiltrate CC chemokine 1
RT generates a potent CC chemokine receptor (CCR)1 and CCR5 agonist with
RT anti-HIV properties.";
RL J. Exp. Med. 192:1051-1058(2000).
CC -I- FUNCTION: Has weak activities on human monocytes and acts via
CC receptors that also recognize MIP-1 alpha. It induced
CC intracellular Ca(2+) changes and enzyme release, but no
CC chemotaxis, at concentrations of 100-1,000 nM, and was inactive on
CC T lymphocytes, neutrophils, and eosinophil leukocytes. Enhances
CC the proliferation of CD34 myeloid progenitor cells. The processed
CC form HCC-1(9-74) is a chemotactic factor that attracts monocytes
CC eosinophils, and T-cells and is a ligand for CCR1, CCR3 and CCR5.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=HCC-1;
CC IsoId=Q16627-1; Sequence=Displayed;
CC Name=HCC-3;
CC IsoId=Q16627-2; Sequence=VSP_001060;
CC -I- TISSUE SPECIFICITY: Expressed constitutively in several normal
CC tissues: spleen, liver, skeletal and heart muscle, gut, and bone
CC marrow, present at high concentrations (1-80 nM) in plasma.
CC -I- PTM: The N-terminal processed forms HCC-1(3-74), HCC-1(4-74) and
CC HCC-1(9-74) are produced in small amounts by proteolytic cleavage
CC after secretion in blood.
CC -I- PTM: HCC-1(1-74), but not HCC-1(3-74) and HCC-1(4-74), is
CC partially O-glycosylated; the O-linked glycan consists of one Gal-
CC GalNAc disaccharide, further modified by two N-acetylneuraminic
CC acids.
CC -I- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.

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CC EMBL; Z49270; CAA89264.1; -;
CC EMBL; Z70292; CAA94307.1; -;
CC EMBL; Z70293; CAA94309.1; -;
CC EMBL; Z49269; CAA89263.1; -;
CC EMBL; AF088219; AAC63329.1; -;
CC EMBL; AF088219; AAF23982.1; -;
CC EMBL; BC045165; AAH45165.1; -;
CC HSSP; P13236; 1HUM.
CC Genew; HGNC:10612; CCL14.
CC MIM; 601392; -;
CC GO; GO:0005615; C:extracellular space; TAS.
CC GO; GO:0004871; F:signal transducer activity; TAS.
CC GO; GO:0006874; P:calcium ion homeostasis; TAS.
CC GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
CC InterPro; IPR000827; CC chemokine sm.
CC InterPro; IPR001811; Chemokine_IL8.
CC Pfam; PF00048; IL8; 1.
CC PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
CC Alternative splicing; Cytokine; Direct protein sequencing;
CC Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 93 Small inducible cytokine A14.
FT CHAIN 22 93 HCC-1(3-74).
FT CHAIN 23 93 HCC-1(4-74).
FT CHAIN 28 59 HCC-1(9-74).
FT DISULFID 35 59 By similarity.

```
FT DISULPID 36 75 By similarity.
FT CARBOHYD 26 26 O-linked (GalNAc...).
FT VARSPLIC 27 27 R -> QTGGKPKVKVQIKLVG (in isoform HCC-
FT 3).
FT
SQ SEQUENCE 93 AA; 10678 MW; DDDDB899DC9148836 CRC64;
Query Match 100.0%; Score 504; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-49;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKISVAAPFLLITIALGKTKTSSSRGPHVPSGCCFTYTKIPRORIMDYETNSQCS 60
Db 1 MKISVAAPFLLITIALGKTKTSSSRGPHVPSGCCFTYTKIPRORIMDYETNSQCS 60
Qy 61 KPGIVFTIKRGHSGVCTNPSPDKVQDYIKDMKEN 93
Db 61 KPGIVFTIKRGHSGVCTNPSPDKVQDYIKDMKEN 93
RESULT 2
Q6DUK4 PRELIMINARY; PRT; 93 AA.
AC Q6DUK4
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Macrophage inflammatory protein 1 alpha.
OS Sus scrofa (pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shirling C.M.A., Takamatsu H.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY643423; AAT65077.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC:chemokine sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 93 AA; 10117 MW; 0B8D26CABE28414C CRC64;
Query Match 51.3%; Score 258.5; DB 2; Length 93;
Best Local Similarity 49.5%; Pred. No. 1.2e-21;
Matches 46; Conservative 22; Mismatches 24; Indels 1; Gaps 1;
Qy 1 MKISVAAPFLLITIALGKTKTSSSRGPHVPSGCCFTYTKIPRORIMDYETNSQCS 60
Db 1 MKVAVALA-ILLCAMALCSQVSPALGADPTACCFSTSRQLPKRFVADYETSSQCS 59
Qy 61 KPGIVFTIKRGHSGVCTNPSPDKVQDYIKDMKEN 93
Db 60 KPGVIFQTKGKGVCANPDAAVQVEYISDLN 92
RESULT 3
SY3L HUMAN STANDARD; PRT; 93 AA.
ID SY3L HUMAN
AC P16619; O96168;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DE Small inducible cytokine A3 like 1 precursor (Tonsillar lymphocyte
DE LD78 beta protein) (LD78-beta(1-70)) (GO/G1 switch regulatory protein
DE 19-2) (GOS19-2 protein) (PAT 464.2) (Contains: LD78-beta(3-70); LD78-
DE beta(5-70)).
GN Names=CCIL3L1; Synonyms=GOS19-2, SCYA3L1;
OS Homo sapiens (Human).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Irving S.G., Zipfel P.F., Baile J., McBride O.W., Morton C.C.,
RX MEDLINE=90287702; PubMed=1972563;
RA Burd P.R., Siebenlist U., Kelly K.;
RT "Two inflammatory mediator cytokine genes are closely linked and
RT variably amplified on chromosome 17q.";
RL Nucleic Acids Res. 18:3261-3270(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91103879; PubMed=22711120;
RA Blum S., Forsdyke R.E., Forsdyke D.R.;
RT "Three human homologs of a murine gene encoding an inhibitor of stem
RT cell proliferation.";
RL DNA Cell Biol. 9:589-602(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=90287155; PubMed=1694014;
RA Nakao M., Nomiya H., Shimada K.;
RT "Structures of human genes coding for cytokine LD78 and their
RT expression.";
RL Mol. Cell. Biol. 10:3646-3658(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 24-38.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [6]
RP IDENTIFICATION OF LD78-BETA(3-70) AND LD78-BETA(5-70), N-TERMINAL
RP PROCESSING, AND FUNCTION.
RX PubMed=10961862;
RA Van Damme J.;
RA Proost P., Menten P., Struyf S., Schuyser E., De Meester I.,
RT "Cleavage by CD26/dipeptidyl peptidase IV converts the chemokine
RT LD78beta into a most efficient monocyte attractant and CCR1 agonist.";
RL Blood 96:1674-1680(2000).
CC -1- FUNCTION: Chemotactic for monocytes. Is a ligand for CCR5.
CC Recombinant small inducible cytokine B10 induces a dose-dependent
CC inhibition of macrophage tropic HIV-1 strains. The processed form
CC LD78-beta(3-70) shows a 20-fold to 30-fold higher chemotactic
CC activity and is also a ligand for CCR1.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: The N-terminal processed forms LD78-beta(3-70) and LD78-
```

```
CC beta(5-70) are produced by proteolytic cleavage after secretion
CC from peripheral blood monocytes. The cleavage to yield LD78-
CC beta(3-70) is probably achieved by DPP4.
CC -I- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC -----
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CC -----
DR EMBL; X52149; CAA36397.1; -
DR EMBL; M24110; AAA35859.1; -
DR EMBL; D90145; EBA14173.1; -
DR EMBL; BC007783; AAH07783.1; -
DR EMBL; BC027888; AAH27888.1; -
DR PIR; B35673; B35673.
DR HSSP; P10147; IB50.
DR Genew; HGNC:10628; CCL3L1.
DR H-InvDB; HIX0020418; -
DR H-InvDB; HIX0023281; -
DR MIM; 601395; -
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0008009; F:chemokine activity; NAS.
DR GO; GO:0006935; P:chemotaxis; NAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Direct protein sequencing; Signal.
FT SIGNAL 1 23
FT CHAIN 24 93 Small inducible cytokine A3 like 1.
FT CHAIN 26 93 LD78-beta(3-70).
FT CHAIN 28 93 LD78-beta(5-70).
FT SITE 25 26 Cleavage (by DPP4) (Probable).
FT DISULFID 34 58 By similarity.
FT DISULFID 35 74 By similarity.
FT CONFLICT 91 91 L -> P (in Ref. 4; AAH07783).
SQ SEQUENCE 93 AA; 10161 MW; A7A79E774006D61E CRC64;

Query Match 47.7%; Score 240.5; DB 1; Length 93;
Best Local Similarity 47.3%; Pred. No. 1.4e-19;
Matches 43; Conservative 22; Mismatches 25; Indels 1; Gaps 1;

QY 1 MKISVAAIPFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60
DB 1 MQVSTAALA-VLLCTMALCNQVLSAPLAADPTACCFSYTSRQIPQNFADYFETSSQCS 59

QY 61 KPGIVFTKRGHVSCTNPSDKWQDYIKDMK 91
DB 60 KPSVIFLTRGRQVCADPSEWQKVYSDLE 90

RESULT 4
ID Q8HYQ3 PRELIMINARY; PRT; 92 AA.
AC Q8HYQ3
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Chemokine CCL3/MIP-1ALPHA.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.

Query Match 47.7%; Score 240.5; DB 1; Length 93;
Best Local Similarity 47.3%; Pred. No. 1.4e-19;
Matches 43; Conservative 22; Mismatches 25; Indels 1; Gaps 1;

QY 1 MKISVAAIPFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60
DB 1 MQVSTAALA-VLLCTMALCNQVLSAPLAADPTACCFSYTSRQIPQNFADYFETSSQCS 59

QY 61 KPGIVFTKRGHVSCTNPSDKWQDYIKDMK 91
DB 60 KPSVIFLTRGRQVCADPSEWQKVYSDLE 90

RESULT 4
ID Q8HYQ3 PRELIMINARY; PRT; 92 AA.
AC Q8HYQ3
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Chemokine CCL3/MIP-1ALPHA.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE-22123042; PubMed-12126650; DOI=10.1006/cyto.2002.0875;
RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
RT "Molecular cloning and sequencing of 25 different rhesus macaque
RT chemokine cDNAs reveals evolutionary conservation among C, CC, CXC,
RT AND CX3C families of chemokines."
RL Cytokine 18:140-148(2002).
DR EMBL; AF449266; AAN76070.1; -
DR HSSP; P10147; IB50.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 92 AA; 10120 MW; 021CAA371143D12A CRC64;

Query Match 47.4%; Score 239; DB 2; Length 92;
Best Local Similarity 48.4%; Pred. No. 2e-19;
Matches 44; Conservative 21; Mismatches 24; Indels 2; Gaps 2;

QY 1 MKISVAAIPFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60
DB 1 MQVSTAALA-VLLCTVALCNRI-SATFAADPTSCCFYSISRQIPQNFADYFETNSQCS 58

QY 61 KPGIVFTKRGHVSCTNPSDKWQDYIKDMK 91
DB 59 KPGVIFLTRGRQVCADPSEWQKVYSDLE 89

RESULT 5
SY03 BOVIN STANDARD; PRT; 93 AA.
ID SY03 BOVIN
AC Q8SQA6;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory
DE protein 1-alpha) (MIP-1-alpha).
GN Name=CCL3; Synonyms=SCYA3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Werling D.;
RT "Role of chemokines in RSV infection.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Monokine with inflammatory and chemokinetic properties.
CC Binds to CCR1, CCR4 and CCR5 [By similarity].
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC -----
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CC -----
DR EMBL; AY077840; AAL78060.1; -
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Inflammatory response; Signal.
FT SIGNAL 1 24 By similarity.
FT CHAIN 25 93 Small inducible cytokine A3.
```


RX PubMed=12401480; DOI=10.1016/S1359-6101(02)00045-X;
RA Menten P., Wuyts A., Van Damme J.;
RT "Macrophage inflammatory protein-1";
RN Cytokine Growth Factor Rev. 13:455-481(2002).
[11]
RP STRUCTURE OF 24-92 BY NMR, AND MUTAGENESIS OF ASP-49 AND GLU-89.
RX PubMed=10347159; DOI=10.1074/jbc.274.23.16077;
RA Czaplinski L.G., McKeating J., Craven C.J., Higgins L.D., Appay V.,
Brown A., Dudgeon T., Howard L.A., Meyers T., Owen J., Palan S.R.,
Tan P., Wilson G., Woods N.R., Heyworth C.M., Lord B.I.,
RA Brotherton D., Christison R., Craig S., Cribbes S., Edwards R.M.,
RA Evans S.J., Gilbert R., Morgan P., Elliot Randle E., Schofield N.,
RA Varley P.G., Fisher J., Jonathan P., Walther J.P., Hunter M.G.;
RT "Identification of amino acid residues critical for aggregation of
human CC chemokines macrophage inflammatory protein (MIP)-1alpha, MIP-
RT 1beta, and RANTES. Characterization of active disaggregated chemokine
RT variants.";
RL J. Biol. Chem. 274:16077-16084(1999).
CC -!- FUNCTION: Monokine with inflammatory and chemokinetic properties.
CC Binds to CCR1, CCR4 and CCR5. One of the major HIV-suppressive
CC factors produced by CD8+ T cells. Recombinant MIP-1-alpha induces
CC a dose-dependent inhibition of different strains of HIV-1, HIV-2,
CC and simian immunodeficiency virus (SIV).
CC -!- SUBUNIT: Self-associates. Also heterodimer of MIP-1-alpha (4-69)
CC and MIP-1-beta(3-69).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: By TPA or PHA (TPA = 12-o-tetradecanoyl phorbol-13
CC acetate (tumor promoter); PHA = phytohemagglutinin (T-cell
CC mitogen)).
CC -!- PTM: N-terminal processed form LD78-alpha(4-69) is produced by
CC proteolytic cleavage after secretion from HTLV1-transformed T-
CC cells.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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CC
DR EMBL; D00044; BAA00029.1; -;
DR EMBL; M23452; AAA36316.1; -;
DR EMBL; M25315; AAA57255.1; -;
DR EMBL; X03754; CAA27388.1; -;
DR EMBL; X04018; CAA27643.1; ALT_SEQ.
DR EMBL; M23178; AAA35858.1; -;
DR EMBL; D90144; BAA14172.1; -;
DR EMBL; AF043339; AAC03539.1; -;
DR PIR; A35673; A30574.
DR PDB; 1B50; NMR; A/B=24-92.
DR PDB; 1B53; NMR; A/B=24-92.
DR Genew; HGNC:10627; CCL3.
DR MIM; 182283; -;
DR GO; GO:0005625; C:soluble fraction; TAS.
DR GO; GO:0008009; F:chemokine activity; TAS.
DR GO; GO:0004871; F:signal transducer activity; TAS.
DR GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . .; TAS.
DR GO; GO:0006874; P:calcium ion homeostasis; TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; TAS.
DR GO; GO:0006887; P:exocytosis; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR GO; GO:0045069; P:regulation of viral genome replication; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR000827; CC_Chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.

KW 3D-structure; Chemotaxis; Cytokine; Direct protein sequencing;
KW Inflammatory response; Signal.
FT SIGNAL 1 23
FT CHAIN 24 92 Small inducible cytokine A3.
FT CHAIN 27 92 MIP-1-alpha(4-69).
FT DISULFID 33 57 By similarity.
FT DISULFID 34 73 By similarity.
FT MUTAGEN 49 49 D->A: Reduces self-association; in BB-
FT 10010: Improved pharmaceutical
FT 10010: Reduces self-association.
FT MUTAGEN 89 89 E->A: Reduces self-association.
FT TURN 44 46
FT STRAND 49 51
FT TURN 55 58
FT STRAND 63 65
FT TURN 67 68
FT TURN 76 77
FT HELIX 79 84
FT TURN 85 88
SQ SEQUENCE 92 AA; 10085 MW; 517865D5D6776CA8 CRC64;
Query Match 46.8%; Score 236; DB 1; Length 92;
Best Local Similarity 48.4%; Pred. No. 4.5e-19;
Matches 44; Conservative 22; Mismatches 23; Indels 2; Gaps 2;
QY 1 MKISVAIPFELLITIALGTCTESSRSGPYHPSECCFTYTYKIPRQIMDYETNSQCS 60
Db 1 MOVSTAAALA-VLCTMALCNQF-SASLAADTTFACFSYTSRQIQNFADIFETSSQCS 58
QY 61 KPGIVFTIKRSHSVCTNPSDKWQDYIKDMK 91
Db 59 KPGVFLTKRSRQVCADPSEEWQKVSDLE 89
RESULT 8
SY04_CHICK STANDARD; PRT; 90 AA.
AC Q04876; Q910C9;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A4 homolog precursor (Macrophage inflammatory
DE protein 1-beta homolog).
GN Name=CCL4; Synonyms=SCY44;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=95369710; PubMed=7642115; DOI=10.1016/0378-1119(95)00210-W;
RA Petrenko O., Ischenko I., Enrietto P.J.;
RT "Isolation of a cDNA encoding a novel chicken chemokine homologous to
RT mammalian macrophage inflammatory protein-1 beta.";
RL Gene 160:305-306(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20049023; PubMed=10582310;
RA Hughes S., Bumstead N.;
RT "Mapping of the gene encoding a chicken homologue of the mammalian
RT chemokine SCY44.";
RL Anim. Genet. 30:404-404(1999).
RN [3]
RP SEQUENCE OF 14-90 FROM N.A.
RA Petrenko O., Enrietto P.J.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Monokine with inflammatory and chemokinetic properties
CC (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L34553; AAA48747.1; -.
DR EMBL; AJ243034; CAB45103.1; -.
DR HSSP; P13236; 1HUM.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemokaxis; Cytokine; Signal.
FT SIGNAL 1 21 By similarity.
FT CHAIN 22 90 Small inducible cytokine A4 homolog.
FT DISULFID 32 56 By similarity.
FT DISULFID 33 72 By similarity.
FT CONFLICT 87 87 M -> L (in Ref. 1).
SQ SEQUENCE 90 AA; 9987 MW; 50AF9679A267408F CRC64;

Query Match 46.7%; Score 235.5; DB 1; Length 90;
Best Local Similarity 47.3%; Pred. No. 5e-19;
Matches 44; Conservative 17; Mismatches 29; Indels 3; Gaps 1;

Qy . 1 MKISVAIPFLLITIALGTETSSRGYPHPSCCFTYTYKIPRQIMDYETNSQCS 60
Db 1 MKUSVAALAVLL---IAICYQTSAAPVGSDDPTSCCFTYISRQLPFSFVADYETNSQCP 57

Qy 61 KPGIVFITRKGHSYCTNPSPDKWQDYIKDMKEN 93
Db 58 HAGVVFITRKGREVCANPQNDWQDYVKNKMLN 90

RESULT 9
Q9PWA6 PRELIMINARY; PRT; 90 AA.
ID O9PWA6
AC O9PWA6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Chemokine.
GN Name=SCYA4;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RL Hughes S.M., Bumstead N.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF146730; AAD48772.1; -.
DR HSSP; P13236; 1HUM.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 90 AA; 9986 MW; 50AF9679A26751CB CRC64;

Query Match 46.7%; Score 235.5; DB 2; Length 90;
Best Local Similarity 47.3%; Pred. No. 5e-19;
Matches 44; Conservative 17; Mismatches 29; Indels 3; Gaps 1;

Qy 1 MKISVAIPFLLITIALGTETSSRGYPHPSCCFTYTYKIPRQIMDYETNSQCS 60
Db 1 MKUSVAALAVLL---IAICYQTSAAPVGSDDPTSCCFTYISRQLPFSFVADYETNSQCP 57
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Db 1 MKUSVAALAVLL---IAICYQTSAAPVGSDDPTSCCFTYISRQLPFSFVADYETNSQCP 57
Qy 61 KPGIVFITRKGHSYCTNPSPDKWQDYIKDMKEN 93
Db 58 HAGVVFITRKGREVCANPQNDWQDYVKNKMLN 90

RESULT 10
SY04 MOUSE STANDARD; PRT; 92 AA.
ID SY04 MOUSE
AC P14097;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory
DE protein 1-beta) (MIP-1-beta) (H400 protein) (SIS-gamma) (ACT2).
GN Name=Ccl4; Synonyms=Mip1b, Scya4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RL MEDLINE=89067830; PubMed=3059856;
RA Sherry B., Tekamp-Olson P., Gallegos C., Bauer D., Davatelis G.,
RA Wolpe S.D., Maslarsz F., Coit D., Cerami A.;
RA "Resolution of the two components of macrophage inflammatory protein
RA 1, and cloning and characterization of one of those components,
RA macrophage inflammatory protein 1 beta.";
RL J. Exp. Med. 168:2251-2259(1988).
RN [2]
RP SEQUENCE FROM N.A.
RL MEDLINE=89093958; PubMed=2521353;
RA Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;
RA "A family of small inducible proteins secreted by leukocytes are
RA members of a new superfamily that includes leukocyte and fibroblast-
RA derived inflammatory agents, growth factors, and indicators of various
RA activation processes.";
RL J. Immunol. 142:679-687(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2J; TISSUE=Liver;
RA Daubersies P., Lepretre F., Bailloul B., Grove M., Pragnell I.,
RA Plumb M.A.;
RL Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.S/J, and SJL/J; TISSUE=Spleen;
RX MEDLINE=99370037; PubMed=10438970;
RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.P., Doerge R.W.,
RA Blankenhorn E.P.;
RT "Sequence polymorphisms in the chemokines Scyal (TCA-3), Scya2
RT (monocyte chemoattractant protein (MCP)-1), and Scyal2 (MCP-5) are
RT candidates for eae7, a locus controlling susceptibility to monophasic
RT remitting/nonrelapsing experimental allergic encephalomyelitis.";
RL J. Immunol. 163:2262-2266(1999).
CC -|- SUBUNIT: Monomer with inflammatory and chemokinetic properties.
CC -|- SUBUNIT: Homodimer (By similarity).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
CC -----
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CC -----
DR EMBL; M23503; AAA40148.1; -.
DR EMBL; M35590; AAA39708.1; -.
DR EMBL; X62502; CAA44364.1; -.
DR EMBL; AF128218; AAF22559.1; -.

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DR EMBL; AF128219; AAF22560.1; -.
DR PIR; C30552; C30552.
DR HSSP; P13236; LHUM.
DR MGD; MGI:98261; Ccl4.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Inflammatory response; Signal.
FT SIGNAL 1 23
FT CHAIN 24 92 Small inducible cytokine A4.
FT DISULFID 34 58 By similarity.
FT DISULFID 35 74 By similarity.
FT DISULFID 35 74 By similarity.
SQ SEQUENCE 92 AA; 10168 MW; 8853FD58FDE61BAC CRC64;

Query Match 46.5%; Score 234.5; DB 1; Length 92;
Best Local Similarity 45.2%; Pred. No. 6.7e-19;
Matches 42; Conservative 20; Mismatches 30; Indels 1; Gaps 1;

QY 1 MKISVAIPFLLITLALGKTSSSRGYPHPSECCFTYTKIPRQIMDYETNSQCS 60
DB 1 MKLCVSALLLLVA-AFCAPGSPMGSDPPTSCCFSTYRSLHRSFVMDYETSLCS 59

QY 61 KPGIVFITKRGHSVCTNPSPDKVQDYIKDMKEN 93
DB 60 KPAVVFITKRGQICANPSPWPWTEYMSDLELN 92

RESULT 11
SY04_RABIT
ID SY04_RABIT STANDARD; PRT; 92 AA.
AC P46632;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory
DE protein 1-beta) (MIP-1-beta) (Immune activation protein 2) (ACT-2).
GN Names=CCL4; Synonyms=SCV4;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white;
RX MEDLINE=94198229; PubMed=8148323;
RA Mori S., Goto K., Goto F., Mutakami K., Ohkawara S., Yoshinaga M.;
RT "Dynamic changes in mRNA expression of neutrophils during the course
RT of acute inflammation in rabbits.";
RL Int. Immunol. 6:149-156(1994).
CC -1- FUNCTION: Monokine with inflammatory and chemokinetic properties
CC (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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CC
CC EMBL; D17402; BAA04226.1; -.
DR EMBL; D17402; BAA04226.1; -.
DR HSSP; P13236; LHUM.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.

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```

KW Chemotaxis; Cytokine; Inflammatory response; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 92 Small inducible cytokine A4.
FT DISULFID 34 58 By similarity.
FT DISULFID 35 74 By similarity.
FT DISULFID 35 74 By similarity.
SQ SEQUENCE 92 AA; 10066 MW; ECBA8818D42A735C CRC64;

Query Match 45.7%; Score 230.5; DB 1; Length 92;
Best Local Similarity 45.2%; Pred. No. 1.9e-18;
Matches 42; Conservative 18; Mismatches 32; Indels 1; Gaps 1;

QY 1 MKISVAIPFLLITLALGKTSSSRGYPHPSECCFTYTKIPRQIMDYETNSQCS 60
DB 1 MKLGVTLSVALLVA-ALCPPALSAPMGSDPPTACCFSTLRKLPFRHFVIDYETSLCS 59

QY 61 KPGIVFITKRGHSVCTNPSPDKVQDYIKDMKEN 93
DB 60 QPAVVFITKRGQVCANPSESWQYVDDLELN 92

RESULT 12
SY04_RAT
ID SY04_RAT STANDARD; PRT; 92 AA.
AC P50230;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory
DE protein 1-beta) (MIP-1-beta).
GN Names=CCL4; Synonyms=Mip1b, Scy44;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Long Evans; TISSUE=Lung;
RA Jones M.L., Shanley T.P., Schmal H., Friedl H.P., Ward P.A.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Monokine with inflammatory and chemokinetic properties.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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CC
CC EMBL; U06434; AAA96497.1; -.
DR HSSP; P13236; LHUM.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Inflammatory response; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 92 Small inducible cytokine A4.
FT DISULFID 34 58 By similarity.
FT DISULFID 35 74 By similarity.
FT DISULFID 35 74 By similarity.
SQ SEQUENCE 92 AA; 10234 MW; 60B451EEBC7103D CRC64;

Query Match 45.5%; Score 229.5; DB 1; Length 92;
Best Local Similarity 44.1%; Pred. No. 2.5e-18;
Matches 41; Conservative 20; Mismatches 31; Indels 1; Gaps 1;

QY 1 MKISVAIPFLLITLALGKTSSSRGYPHPSECCFTYTKIPRQIMDYETNSQCS 60
DB 1 MKLCVSALLLLVA-AFCDSVLSAPIGSDPPTSCCFSTYRSLHRSFVMDYETSLCS 59

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Qy 61 KPGIVFITKRGHSVCTNPDSKXVDQYIKDMKEN 93
   : : |||:| | : | : |||: | | : | : | : |
Db 60 QPAVVFTTKGRQICADSEPVNVEYVNDLELN 92

RESULT 13
Q8HYQ2 PRELIMINARY; PRT; 92 AA.
ID Q8HYQ2 AC Q8HYQ2;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Chemokine CCL4/MIP-1BETA.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2213042; PubMed=12126650; DOI=10.1006/cyto.2002.0875;
RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
RT "Molecular cloning and sequencing of 25 different rhesus macaque
RT chemokine cDNAs reveals evolutionary conservation among C, CC, CXC,
RT AND CX3C families of chemokines.";
RL Cycokine 18:140-148 (2002).
DR EMBL; AF449267; AAN76071.1; -.
DR . HSSP; P13236; 1HUM.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemkine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
DR SEQUENCE 92 AA; 10103 MW; 80B2C2071565F809 CRC64;

Query Match 45.5%; Score 229.5; DB 2; Length 92;
Best Local Similarity 44.1%; Pred. No. 2.5e-18;
Matches 41; Conservative 20; Mismatches 31; Indels 1; Gaps 1;

Qy 1 MKISVAALPPFLITIALGTKESSRGYPHPSCCTTYTYKIPQRIMDYVETNSQCS 60
   |||:| | : | : |||:| | : | : |||:| | : | : |||:| |
Db 1 MKLCVTVLIS-LLVLAAPFCSPALAPMGSDPPTSCFSYARKLPFRNFVVDYETSLCS 59

Qy 61 KPGIVFITKRGHSVCTNPDSKXVDQYIKDMKEN 93
   : : |||:| | : | : |||:| | : | : |||:| |
Db 60 QPAVVFTTKGRQICADSEPVNVEYVNDLELN 92

RESULT 14
Q8NHW4 PRELIMINARY; PRT; 92 AA.
ID Q8NHW4 AC Q8NHW4;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Macrophage inflammatory protein-1b2.
GN Name=CCL4L1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Nibbs R.J., Barcellos L.F., Townsend J.R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY079147; AAL87008.1; -.
DR PIR; C60407; C60407.
DR HSSP; P13236; 1HUM.
DR GO; GO:0005576; C:extracellular; IEA.

```

[Contains: MIP-1-beta(3-69)].
GN Name=CCl4; Synonyms=LAG1, MIP1B, SCVA4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=89071764; PubMed=2462251;
RA Lipas M.A., Napolitano M., Jeang K.-T., Chang N.T., Leonard W.J.;
RT "Identification, cloning, and characterization of an immune activation
RT gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:9704-9708(1988).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=89140347; PubMed=2521882;
RA Zipfel P.F., Balke J., Irving S.G., Kelly K., Siebenlist U.;
RT "Mitogenic activation of human T cells induces two closely related
RT genes which share structural similarities with a new family of
RT secreted factors.";
RL J. Immunol. 142:1582-1590(1989).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=89093958; PubMed=2521353;
RA Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;
RT "A family of small inducible proteins secreted by leukocytes are
RT members of a new superfamily that includes leukocyte and fibroblast-
RT derived inflammatory agents, growth factors, and indicators of various
RT activation processes.";
RL J. Immunol. 142:679-687(1989).
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE=91061800; PubMed=2247088; DOI=10.1016/0161-5890(90)90097-J;
RA Baixeras E., Roman-Roman S., Jitsukawa S., Genevee C., Mechiche S.,
RA Viegas-Pequignot E., Hercend T., Triebel F.;
RT "Cloning and expression of a lymphocyte activation gene (LAG-1).";
RL Mol. Immunol. 27:1091-1102(1990).
RN [5]
RN SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=89325421; PubMed=2568930;
RA Chang H.C., Reinherz E.L.;
RT "Isolation and characterization of a cDNA encoding a putative cytokine
RT which is induced by stimulation via the CD2 structure on human T
RT lymphocytes.";
RL Eur. J. Immunol. 19:1045-1051(1989).
RN [6]
RN SEQUENCE FROM N.A.
RX MEDLINE=91373378; PubMed=1894635;
RA Napolitano M., Modi W.S., Cevalero S.J., Gnarr J.R., Seuanez H.N.,
RA Leonard W.J.;
RT "The gene encoding the Act-2 cytokine. Genomic structure, HTLV-I/Tax
RT responsiveness of 5' upstream sequences, and chromosomal
RT localization.";
RL J. Biol. Chem. 266:17531-17536(1991).
RN [7]
RN SEQUENCE FROM N.A.
RA Birren B., Fasman K., McKernan K., Nusbaum C., Richardson P.,
RA Lander E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [8]
RN SEQUENCE OF 6-92 FROM N.A.
RX MEDLINE=90038522; PubMed=2809212;
RA Miller M.D., Hata S., Waal Malefyt R., Krangel M.S.;
RT "A novel polypeptide secreted by activated human T lymphocytes.";
RL J. Immunol. 143:2907-2916(1989).
RN [9]
RN RECEPTOR INTERACTION.
RX MEDLINE=98180363; PubMed=9521068;
RX DOI=10.1002/(SICI)1521-4141(199802)28:02<582::AID-IMMU582>3.3.CO;2-1;
RA Bernardini G., Hedrick J.J., Sorzani S., Iulini W., Spinetti G.,
RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
RA Napolitano M.;

RT "Identification of the CC chemokines TARC and macrophage inflammatory
RT protein-1 beta as novel functional ligands for the CCR8 receptor.";
RL Eur. J. Immunol. 28:582-588(1998).
RN [10]
RN FUNCTION.
RX MEDLINE=96106406; PubMed=8525373;
RA Cocchi F., DeVico A.L., Garzino-Demo A., Arya S.K., Gallo R.C.,
RA Lusso P.;
RT "Identification of RANTES, MIP-1 alpha, and MIP-1 beta as the major
RT HIV-suppressive factors produced by CD8+ T cells.";
RL Science 270:1811-1815(1995).
RN [11]
RN IDENTIFICATION OF MIP-1-BETA(3-69) BY MASS SPECTROMETRY, FUNCTION, AND
RX SUBUNIT.
RX PubMed=12070155; DOI=10.1074/jbc.M203077200;
RA Guan E., Wang J., Roderiquez G., Norcross M.A.;
RT "Natural truncation of the chemokine MIP-1beta /CCL4 affects receptor
RT specificity but not anti-HIV-1 activity.";
RL J. Biol. Chem. 277:32348-32352(2002).
RN [12]
RN REVIEW.
RX PubMed=12401480; DOI=10.1016/S1359-6101(02)00045-X;
RA Menten P., Wuyts A., Van Damme J.;
RT "Macrophage inflammatory protein-1.";
RL Cytokine Growth Factor Rev. 13:455-481(2002).
RN [13]
RN STRUCTURE BY NMR.
RX MEDLINE=94182137; PubMed=8134838;
RA Lodi P.J., Garrett D.S., Kuscewski J., Taang M.L.S., Weatherbee J.A.,
RA Leonard W.J., Gronenborn A.M., Clore G.M.;
RT "High-resolution solution structure of the beta chemokine hMIP-1 beta
RT by multidimensional NMR.";
RL Science 263:1762-1767(1994).
CC -!- FUNCTION: Monokine with inflammatory and chemokinetic properties.
CC Binds to CCR5 and to CCR8. One of the major HIV-suppressive
CC factors produced by CD8+ T cells. Recombinant MIP-1-beta induces a
CC dose-dependent inhibition of different strains of HIV-1, HIV-2,
CC and simian immunodeficiency virus (SIV). The processed form MIP-1-
CC beta(3-69) retains the abilities to induce down-modulation of
CC surface expression of the chemokine receptor CCR5 and to inhibit
CC the CCR5-mediated entry of HIV-1 in T cells. MIP-1-beta(3-69) is
CC also a ligand for CCR1 and CCR2 isoform B.
CC -!- SUBUNIT: Homodimer and heterodimer of MIP-1-alpha(4-69) and MIP-1-
CC beta(3-69).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: By mitogens.
CC -!- PTM: N-terminal processed form MIP-1-beta(3-69) is produced by
CC proteolytic cleavage after secretion from peripheral blood
CC lymphocytes.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC -----
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CC -----
CC EMBL; M23502; AAA36656.1; -
CC EMBL; M25316; AAA57256.1; -
CC EMBL; J04130; AAA51576.1; -
CC EMBL; X51683; CAA37723.1; -
CC EMBL; X53682; CAA37722.2; ALT_SEQ.
CC EMBL; X16166; CAA34231.1; -
CC EMBL; M69203; AAB00790.1; -
CC EMBL; M69201; AAB00790.1; JOINED.
CC EMBL; M69202; AAB00790.1; JOINED.
CC EMBL; AC003976; -; NOT ANNOTATED_CDS.
CC EMBL; M57503; AAA36752.1; -
CC PIR; JH0319; A31767.
CC PDB; 1HUN; NMR; A/B=24-92.
CC PDB; 1HUN; NMR; A/B=24-92.

PDB; 1JE4; NMR; A=24-92.
DR GEM; HGNC:10630; CCL4.
DR MIN; 182284; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0008009; P:chemokine activity; TAS.
DR GO; GO:0047116; P:receptor signaling protein tyrosine kinase . . . ; TAS.
DR GO; GO:0007155; P:cell adhesion; TAS.
DR GO; GO:0008131; P:cell growth and/or maintenance; TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007163; P:establishment and/or maintenance of cell po. . . ; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR GO; GO:0009615; P:response to virus; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR GO; GO:0019079; P:viral genome replication; TAS.
DR InterPro; IPR000827; CC chemokine sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00472; SMALL CYTOKINES CC; 1.
KW 3D-structure; Chemotaxis; Cytokine; Inflammatory response; Signal.
FT SIGNAL 1 23 Small inducible cytokine A4.
FT CHAIN 24 92 MIP-1-beta(3-69).
FT * CHAIN 26 92 By similarity.
FT DISULFID 34 58 By similarity.
FT * DISULFID 35 74 By similarity.
FT * CONFLICT 6 6 T -> C (in Ref. 7).
FT CONFLICT 15 15 A -> S (in Ref. 6).
FT CONFLICT 20 20 P -> L (in Ref. 2).
FT CONFLICT 40 45 ARKLP -> REAS (in Ref. 3).
FT CONFLICT 56 56 S -> I (in Ref. 8).
FT CONFLICT 70 70 S -> G (in Ref. 6).
FT CONFLICT 80 80 S -> T (in Ref. 7 and 8).
FT STRAND 29 29
FT STRAND 33 33
FT HELIX 45 47
FT STRAND 50 53
FT STRAND 63 66
FT STRAND 72 75
FT TURN 77 78
FT HELIX 80 92
SQ SEQUENCE 92 AA; 10212 MW; F2EA7CF341B0F258 CRC64;
Query Match 44.5%; Score 224.5; DB 1; Length 92;
Best Local Similarity 43.0%; Pred. No. 9.3e-18;
Matches 40; Conservative 20; Mismatches 32; Indels 1; Gaps 1;
Qy 1 MKISVAIPFLLITIALGTKESSRGPHSPSCCTTYTKIPRORIMDYETNSQCS 60
Db 1 MKLCVTVLSLLVLA-AFCSPALAPMGSDPPTACCFSTARKLPNRFVVDYETSLCS 59
Qy 61 KPGIVFTKRGHVCNTNPDKWQDYIKDMKEN 93
Db 60 QPAVVFQTKRGKQVCADPSESQVQYVDLELN 92
RESULT 17
Q6NSB0 PRELIMINARY; PRT; 92 AA.
AC Q6NSB0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chemokine (C-C motif) ligand 4-like 1.
GN Name=CCL4l1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pooled;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pooled;
RA Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC070310; AAH70310.1; -.
DR HSSP; P10147; 1B50.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC chemokine sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00472; SMALL CYTOKINES CC; 1.
SQ SEQUENCE 92 AA; 10147 MW; 6A567D8926CDE89F CRC64;
Query Match 44.3%; Score 223.5; DB 2; Length 92;
Best Local Similarity 43.0%; Pred. No. 1.2e-17;
Matches 40; Conservative 20; Mismatches 32; Indels 1; Gaps 1;
Qy 1 MKISVAIPFLLITIALGTKESSRGPHSPSCCTTYTKIPRORIMDYETNSQCS 60
Db 1 MKLCVTVLSLLVLA-AFCSPALAPMGSDPPTACCFSTARKLPNRFVVDYETSLCS 59
Qy 61 KPGIVFTKRGHVCNTNPDKWQDYIKDMKEN 93
Db 60 QPAVVFQTKRGKQVCADPSESQVQYVDLELN 92
RESULT 18
SY03 MOUSE
ID SY03 MOUSE STANDARD; PRT; 92 AA.
AC P10855; P14096;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory
DE protein 1-alpha) (MIP-1-alpha) (TY-5) (SIS-alpha) (Heparin-binding
DE chemotaxis protein) (L2G25B).
GN Name=Ccl3; Synonyms=Mipla, Scy3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88258380; PubMed=3290382;
RA Davatelis G., Tekamp-Olson P., Wolpe S.D., Hermens K., Luedke C.,
RA Gallegos C., Coit D., Merryweather J., Cerami A.;
RT "Cloning and characterization of a cDNA for murine macrophage
RT inflammatory protein (MIP), a novel monokine with inflammatory and

chemokinetic properties.";
J. Exp. Med. 167:1939-1944(1988).
[2]
REVISIONS.
Davatelis G., Tekamp-Olson P., Wolpe S.D., Hermesen K., Luedke C.,
Gallejos C., Colt D., Merryweather J., Cerami A.;
J. Exp. Med. 170:2189-2189(1989).
[3]
SEQUENCE FROM N.A.
MEDLINE=89093958; PubMed=2521353;
Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;
"A family of small inducible proteins secreted by leukocytes are
members of a new superfamily that includes leukocyte and fibroblast-
derived inflammatory agents, growth factors, and indicators of various
activation processes.";
J. Immunol. 142:679-687(1989).
[4]
SEQUENCE FROM N.A.
RC STRAIN=DBA/2J;
MEDLINE=91016858; PubMed=2216738;
Grove M., Lowe S., Graham G., Pragnell I., Plumb M.;
"Sequence of the murine haemopoietic stem cell inhibitor/macrophage
inflammatory protein-1 alpha gene.";
Nucleic Acids Res. 18:5561-5561(1990).
[5]
SEQUENCE FROM N.A.
RC MEDLINE=89184547; PubMed=2784565;
Kwon B.S., Weissman S.M.;
"CDNA sequences of two inducible T-cell genes.";
Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).
[6]
SEQUENCE FROM N.A.
RC MEDLINE=91271116; PubMed=2033269;
Widmer U., Yang Z., van Deventer S., Manogue K.R., Sherry B.,
Cerami A.;
"Genomic structure of murine macrophage inflammatory protein-1 alpha
and conservation of potential regulatory sequences with a human
homolog, LD78.";
J. Immunol. 146:4031-4040(1991).
[7]
SEQUENCE FROM N.A.
RC STRAIN=B10.S/J, BALB/cJ, DBA/2J, NOD/LtJ, and SJL/J; TISSUE=Spleen;
MEDLINE=99370037; PubMed=10438970;
Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
Blankenhorn E.P.;
"Sequence polymorphisms in the chemokines Sca1 (TCA-3), Sca2
(monocyte chemoattractant protein (MCP)-1), and Sca12 (MCP-5) are
candidates for eae7, a locus controlling susceptibility to monophasic
remitting/nonrelapsing experimental allergic encephalomyelitis.";
J. Immunol. 163:2262-2266(1999).
[8]
SEQUENCE OF 24-42.
RC MEDLINE=88154745; PubMed=3279154;
Wolpe S.D., Davatelis G., Sherry B., Beutler B., Hesse D.G.,
Nguyen H.T., Moldaver L.L., Nathan C.F., Lowry S.F., Cerami A.;
"Macrophages secrete a novel heparin-binding protein with inflammatory
and neutrophil chemokinetic properties.";
J. Exp. Med. 167:570-581(1988).
CC -1- FUNCTION: Monokine with inflammatory, pyrogenic and chemokinetic
properties. Has a potent chemotactic activity for eosinophils.
CC Binding to a high-affinity receptor activates calcium release in
neutrophils.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed in lung, spleen, and pancreas.
CC -1- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.

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CC or send an email to license@isb-sib.ch).

CC EMBL; M23447; AAA40146.1; -
DR EMBL; X12531; CAA31047.1; -
DR EMBL; X53372; CAA37452.1; -
DR EMBL; J04451; AAA40304.1; -
DR EMBL; M73061; AAA39707.1; -
DR EMBL; AF065939; AAC17506.1; -
DR EMBL; AF065940; AAC17507.1; -
DR EMBL; AF065941; AAC17508.1; -
DR EMBL; AF065942; AAC17509.1; -
DR EMBL; AF065943; AAC17510.1; -
DR PIR; S11685; A32393.
DR HSSP; P10147; 1B50.
DR MGD; MGI:98260; Ccl3.
DR GO; GO:000809; F:chemokine activity; IDA.
DR InterPro; IPR000827; CC_chemokine_emi.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Direct protein sequencing;
KW Inflammatory response; Signal.
FT SIGNAL 1 23
FT CHAIN 24 92 Small inducible cytokine A3.
FT DISULFID 34 57 By similarity.
FT DISULFID 35 73 By similarity.
FT CONFLICT 22 22 F -> L (in Ref. 3).
FT CONFLICT 62 62 V -> A (in Ref. 3).
SQ SEQUENCE 92 AA; 10345 MW; 8BFF2DE7C6DEDD38 CRC64;

Query Match 44.2%; Score 223; DB 1; Length 92;
Best Local Similarity 45.2%; Pred. No. 1.4e-17;
Matches 42; Conservative 21; Mismatches 28; Indels 2; Gaps 2;

QY 1 MKISVAIPFFLLITLCTKTESSSRGYPHSECCFTTYTKIPQRIMDYETNSQCS 60
DB 1 MKVSTTALA-VLLCTMTLCNQVFSAPYGADTPTACCFYSR-KIPRQFIVDFETSSLCS 58

QY 61 KPGIVFTRKGRHSVCTNPDSKVVQDYIKDMKEN 93
DB 59 QPGVFLTRKQICADSKETWVQEVITDLELN 91

RESULT 19
SV03 RAT STANDARD; PRT; 92 AA.
ID SV03 RAT STANDARD; PRT; 92 AA.
AC P50229;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory
protein 1-alpha) [MIP-1-alpha].
DE Name=Ccl3; Synonyms=Mipia, Sca3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=95298037; PubMed=7779098;
RA Shi M.M., Godleski J.J., Paulauskis J.D.;
RT "Molecular cloning and posttranscriptional regulation of macrophage
inflammatory protein-1 alpha in alveolar macrophages.";
RL Biochem. Biophys. Res. Commun. 211:289-295(1995).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Long Evans; TISSUE=Lung;
RX MEDLINE=95238980; PubMed=772328;
RA Shanley T.P., Schmal H., Friedl H.P., Jones M.L., Ward P.A.;
RT "Role of macrophage inflammatory protein-1 alpha (MIP-1 alpha) in
acute lung injury in rats.";
RL J. Immunol. 154:4793-4802(1995).
RN [3]

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RP SEQUENCE OF 24-57.
RC STRAIN=Wistar;
RX MEDLINE=96183056; PubMed=8607872; DOI=10.1006/bbrc.1996.0511;
RA Nakagawa H., Shota S., Takano K., Shibata F., Kato H.;
RT "Cytokine-induced neutrophil chemoattractant (CINC)-2 alpha, a novel
RT member of rat GRO/CINC, is a predominant chemokine produced by
RT lipopolysaccharide-stimulated rat macrophages in culture.";
RL Biochem. Biophys. Res. Commun. 220:945-948(1996).
CC -1- FUNCTION: Monokine with inflammatory and chemokinetic properties.
CC Has chemotactic activity for monocytes, neutrophils, eosinophils,
CC basophils, and lymphocytes. Required for lung TNF-alpha
CC production, neutrophil recruitment and subsequent lung injury and
CC may function as an autocrine mediator for the macrophage
CC production of TNF-alpha which in turn up-regulates vascular
CC adhesion molecules required for neutrophil influx. This protein
CC binds heparin.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- INDUCTION: By lipopolysaccharide (LPS).
CC -1- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
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DR EMBL; U22414; AAA80608.1; -.
DR EMBL; U06435; AAA96498.1; -.
DR PIR; I52322; I52322.
DR HSP; P10147; I850.
DR RGD; 3647; CCL3.
DR InterPro; IPR000827; CC chemokine sm1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Direct protein sequencing; Heparin-binding;
KW Inflammatory response; Signal.
FT SIGNAL 1 23
FT CHAIN 24 92 Small inducible cytokine A3.
FT DISULFID 34 57 By similarity.
FT DISULFID 35 73 By similarity.
FT CONFLICT 6 6 A -> T (in Ref. 2).
FT CONFLICT 57 57 C -> W (in Ref. 2 and 3).
SQ SEQUENCE 92 AA; 10335 MW; 14B861C647F9A2EB CRC64;
Query Match 44.2%; Score 223; DB 1; Length 92;
Best Local Similarity 45.2%; Pred. No. 1.4e-17;
Matches 42; Conservative 22; Mismatches 27; Indels 2; Gaps 2;
QY 1 MKISVAAIPFFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60
DB 1 MKYSTAALA-VLLCTMALNVEVFSAPYGADTPACCFSGYGR-QIPRKFADYFETSLCS 58
QY 61 KPGIVFTKRGHSVCTNPSDKWQDYIKDKMEN 93
DB 59 QPGVIFLTKRNRQICADPKETWQYETILELN 91
RESULT 20
Q91ZLO PRELIMINARY; PRT; 92 AA.
AC Q91ZLO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Macrophage inflammatory protein 1 beta.
GN Name=IP-1beta;
OS Sigmmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmmodontinae;
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OC Sigmmodon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22079879; PubMed=12085325;
RA Blanco J.C., Richardson J.Y., Darnell M.E., Rowzee A., Pletneva L.,
RA Porter D.D., Prince G.A.;
RT "Cytokine and chemokine gene expression after primary and secondary
RT respiratory syncytial virus infection in cotton rats.";
RL J. Infect. Dis. 185:1780-1785(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=1498081; DOI=10.1089/10799900477219873;
RA Blanco J.C., Pletneva L., Boukhalova M., Richardson J.Y.,
RA Harris K.A., Prince G.A.;
RT "The cotton rat: an underutilized animal model for human infectious
RT diseases can now be exploited using specific reagents to cytokines,
RT chemokines, and interferons.";
RL J. Interferon Cytokine Res. 24:21-28(2004).
DR EMBL; AF421392; AAL16933.1; -.
DR HSP; P13236; IHUM.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCV; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 92 AA; 10195 MW; A34FDE21E6FA9C2B CRC64;
Query Match 44.1%; Score 222.5; DB 2; Length 92;
Best Local Similarity 41.9%; Pred. No. 1.6e-17;
Matches 39; Conservative 20; Mismatches 33; Indels 1; Gaps 1;
QY 1 MKISVAAIPFFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60
DB 1 MKLCLSTALLALLAEFCAPVT-SAPRGSPPPICSCFSVASRKLPRNFVDYVETSLCS 59
QY 61 KPGIVFTKRGHSVCTNPSDKWQDYIKDKMEN 93
DB 60 KPAVVELTRKGEVCADPSQPVWYVNDLELN 92
RESULT 21
Q68A92 PRELIMINARY; PRT; 92 AA.
AC Q68A92;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DS CC chemokine ligand 3.
GN Name=CCL3;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Teukui T., Sakaguchi M., Maeda S., Koyanagi M., Masuda K., Ohno K.,
RA Tsujimoto H., Iwabuchi S.;
RT "Expression analysis of gene in canine atopic dermatitis.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB164618; BAD42447.1; -.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCV; 1.
SQ SEQUENCE 92 AA; 10029 MW; 9D44596B37FD6910 CRC64;
Query Match 43.7%; Score 220; DB 2; Length 92;
Best Local Similarity 47.3%; Pred. No. 3e-17;
Matches 43; Conservative 20; Mismatches 26; Indels 2; Gaps 2;
QY 1 MKISVAAIPFFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60
DB 1 MKISVAAIPFFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60
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Db	1	MKVPGAALA-VLLCTMSLCSQV-FSPFGADTPIACCSFVSVKQIPRKFIWDCFETSSQCS	58
QY	61	KPGIVFTIKRGHVSCTNPSPKQWQDYIKDMK	91
Db	59	KPGIIFETKRGQACANPSEAWQVQYVADLK	89
RESULT 22			
Q80XG5	Q80XG5	PRELIMINARY;	PRT; 85 AA.
AC	Q80XG5;		
DT	01-JUN-2003 (TREMBLrel. 24, Created)		
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	CC chemokine ligand 4 (Fragment).		
GN	Names=Ccl4;		
OS	Peromyscus maniculatus (Deer mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;		
OC	Peromyscus.		
OX	NCBI_TaxID=10042;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Schountz T., Buniger A., Davenport B., Hegg T.;		
RT	"Cloning of deer mouse IL-2, IL-12 p35, IL-21, GM-CSF, CCL3 and CCL4		
RT	cDNAs."		
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY247758; AAP04417.1; -.		
DR	HSSP; P13236; IHUM.		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0008009; F:chemokine activity; IEA.		
DR	GO; GO:0006955; P:immune response; IEA.		
DR	InterPro; IPR000827; CC_chemkine_sml.		
DR	InterPro; IPR001811; Chemokine_IL8.		
DR	Pfam; PF00048; IL8; 1.		
DR	SMART; SM00199; SCY; 1.		
DR	PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.		
FT	NON_TER	85	
SQ	SEQUENCE	85 AA; 9345 MW; B87216EB9B41F34C	CRC64;
Query Match 43.2%; Score 217.5; DB 2; Length 85;			
Best Local Similarity 45.3%; Pred. No. 5.4e-17;			
Matches 39; Conservative 17; Mismatches 29; Indels 1; Gaps 1;			
QY	1	MKISVAIPFLITLALGCTKTSSSRGPVHPSECCFTYTYKIPRQIMDYVETNSQCS	60
Db	1	MKLCVSALSFLVVA-AFWAPALSAPMGDPPTSCCFSTYARKLPRNFVTDYVETSSLCS	59
QY	61	KPGIVFTIKRGHVSCTNPSPKQWQDY	86
Db	60	KPAVFLTRKGKQVADPSPWPWNEY	85
RESULT 23			
Q14745	Q14745	PRELIMINARY;	PRT; 80 AA.
AC	Q14745;		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
DE	LD78 alpha beta precursor (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RA	Ishizuka K., Igata-Yi R., Naruse K., Nakashima H., Ohuchi K.,		
RA	Katsuragi S., Kin Y., Ohmoto Y., Nomiya H., Iio M., Miura R.,		
RA	Miyakawa T.;		
RL	Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; D63785; BAA09855.1; -.		
DR	HSSP; P10147; IB50.		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0008009; F:chemokine activity; IEA.		
DR	GO; GO:0006955; P:immune response; IEA.		
DR	InterPro; IPR000827; CC_chemkine_sml.		
DR	InterPro; IPR001811; Chemokine_IL8.		
DR	Pfam; PF00048; IL8; 1.		
DR	SMART; SM00199; SCY; 1.		
DR	PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.		
FT	NON_TER	1	
SQ	SEQUENCE	56 AA; 6442 MW; EB12A0E0D41D6F68	CRC64;
Query Match 41.5%; Score 209; DB 2; Length 56;			
Best Local Similarity 57.1%; Pred. No. 3.3e-16;			
Matches 32; Conservative 14; Mismatches 10; Indels 0; Gaps 0;			
QY	32	PSECCFTYTYKIPRQIMDYVETNSQCSKPGIVFTIKRGHVSCTNPSPKQWQDYI	87
Db	1	PTACCSYTSROIQNFIADYFETSSQCSKPGIVFTIKRSRQVADPSEWQKIV	56

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RESULT 25
Q918E0 PRELIMINARY; PRT; 89 AA.
ID Q918E0
AC Q918E0
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Chemokine K203 precursor.
GN Name=K203;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20170941; PubMed=10704244; DOI=10.1006/cyto.1999.0543;
RA Sick C., Schneider K., Staeheli P., Weining K.C.;
RT "Novel chicken CXCR and CC chemokines."
RL EMBL; Y18692; CAB70956.1; -.
DR HSSP; Q16663; 2HCC.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
KW Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 89 Chemokine K203.
SQ SEQUENCE 89 AA; 9896 MW; 6FA2EA7A4950CA75 CRC64;

Query Match 41.5%; Score 209; DB 2; Length 89;
Best Local Similarity 43.0%; Pred. No. 5.3e-16;
Matches 40; Conservative 18; Mismatches 31; Indels 4; Gaps 2;

Qy 1 MKISVAIPPELLITIALGTKESSRGYPHPSCCTTYTYKIPRQIMDYETNSQCS 60
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1 MKLSAVVL--ALLIASFCSSASSAPVGPDPVT-CCTTYTHKIPRNLQIRHYSTSCS 56

Qy 61 KPGIVFTKRGHSVCTNPSPDWQDYIKDMKEN 93
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 57 KPAIFITTKEREVCANPDPWPVQYLSQVKRD 89

RESULT 26
SY18_HUMAN STANDARD; PRT; 89 AA.
ID SY18_HUMAN
AC P55774;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Small inducible cytokine A18 precursor (CC118) (Macrophage
DE inflammatory protein 4) (MIP-4) (Pulmonary and activation-regulated
DE chemokine) (CC chemokine PARC) (Alternative macrophage activation-
DE associated CC chemokine 1) (AMAC-1) (Dendritic cell chemokine 1) (DC-
DE CK1).
GN Name=CCL18; Synonyms=AMAC1, DCC1, MIP4, PARC, SCYA18;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li H., Ruben S.;
RT "Macrophage inflammatory protein-3 and -4."
RL Patent number US5504003, 02-APR-1996.
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Aorta, and Lung;
RX MEDLINE=97376836; PubMed=9233607;

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RA Hieshima K., Imai T., Baba M., Shoudai K., Ishizuka K., Nakagawa T.,
RA Tsuruta J., Takeya M., Sakaki Y., Takatsuki K., Miura R.,
RA Odenakker G., van Damme J., Yoshie O., Nomiya H.;
RT "A novel human CC chemokine PARC that is most homologous to
RT macrophage-inflammatory protein-1 alpha/LD78 alpha and chemotactic for
RT T lymphocytes, but not for monocytes."
RL J. Immunol. 159:1140-1149(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98230488; PubMed=9570561;
RA Kodelja V., Mueller C., Politz O., Haki N., Orfanos C.E., Goerd S.;
RT "Alternative macrophage activation-associated CC-chemokine-1, a novel
RT structural homologue of macrophage inflammatory protein-1 alpha with a
RT Th2-associated expression pattern."
RL J. Immunol. 160:1411-1418(1998).
RN [4]
RP DISCUSSION OF SEQUENCE.
RX MEDLINE=97275308; PubMed=9129202;
RA Wells T.N.C., Peitsch M.C.;
RT "The chemokine information source: identification and characterization
RT of novel chemokines using the WorldWideWeb and expressed sequence tag
RT databases."
RL J. Leukoc. Biol. 61:545-550(1997).
RN [5]
RP SEQUENCE FROM N.A., AND SEQUENCE OF N-TERMINUS.
RC TISSUE=Dendritic cell;
RX MEDLINE=97336102; PubMed=912897; DOI=10.1038/42716;
RA Adema G.J., Hartgers F., Verstraten R., de Vries E., Marland G.,
RA Menon S., Foster J., Xu Y., Nooyen P., McClanahan T., Bacon K.B.,
RA Figdor C.G.;
RT "A dendritic-cell-derived C-C chemokine that preferentially attracts
RT naive T cells."
RL Nature 387:713-717(1997).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=99168908; PubMed=10049593; DOI=10.1006/geno.1998.5670;
RA Tsaaki Y., Fukuda S., Iio M., Miura R., Inai T., Sugano S., Yoshie O.,
RA Hughes A.L., Nomiya H.;
RT "Chemokine PARC gene (SCYA18) generated by fusion of two MIP-
RT 1alpha/LD78alpha-like genes."
RL Genomics 55:353-357(1999).
RN [7]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=99189237; PubMed=10087196; DOI=10.1006/geno.1998.5635;
RA Guan P., Burghes A.H.M., Cunningham A., Lira P., Briessette W.H.,
RA Neote K., McCall S.R.;
RT "Genomic organization and biological characterization of the novel
RT human CC chemokine DC-CK-1/PARC/MIP-4/SCYA18."
RL Genomics 56:296-302(1999).
RN [8]
RP SEQUENCE FROM N.A.
RA Politz O., Kodelja V., Guillot P., Orfanos C.E., Goerd S.;
RT "The genomic locus for the AMAC-1 gene contains possible pseudo-exons
RT within the first intron sequence."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Chemotactic factor that attracts lymphocytes but not
CC monocytes or granulocytes. May be involved in B cell migration
CC into B cell follicles in lymph nodes. Attracts naive T lymphocytes
CC toward dendritic cells and activated macrophages in lymph nodes.
CC has chemotactic activity for naive T cells, CD4+ and CD8+ T cells
CC and thus may play a role in both humoral and cell-mediated
CC immunity responses.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed at high levels in lung, lymph nodes,
CC placenta, bone marrow, dendritic cells present in germinal centers
CC and T-cell areas of secondary lymphoid organs and macrophages
CC derived from peripheral blood monocytes. Not expressed by
CC peripheral blood monocytes and a monocyte-to-macrophage
CC differentiation is a prerequisite for expression.
CC -1- INDUCTION: Specifically induced in macrophages by IL-4, IL-13, and
CC IL-10. Expression is inhibited by IFN-gamma while glucocorticoids
CC exert a slightly positive synergistic effect in combination with
CC IL-4. Strongly induced in several human cell lines, including

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DR EMBL; U58913; AAD10846.1; -.
DR EMBL; U67128; AAD00161.1; -.
DR EMBL; AF088219; AAC63326.1; -.
DR EMBL; AF088219; AAC63327.1; -.
DR PDB; 1C9L; NMR; A=44-120.
DR Genew; HGNC:10622; CCL23.
DR MIM; 602494; -.
DR GO; GO:0008009; F:chemokine activity; TAS.
DR GO; GO:0006874; P:calcium ion homeostasis; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW 3D-structure; Alternative splicing; Chemotaxis; Cytokine;
KW direct protein sequencing; Heparin-binding; Inflammatory response;
KW polymorphism; Signal.
FT SIGNAL 1 21
FT CHAIN 22 120 Small inducible cytokine A23.
FT DISULFID 54 78
FT DISULFID 55 94
FT DISULFID 65 105
FT VARSPIC 46 46
FT VARIANT 106 106
FT CONFLICT 12 44
FT STRAND 58 58
FT HELIX 65 67
FT STRAND 70 73
FT TURN 76 77
FT STRAND 83 86
FT TURN 88 89
FT STRAND 92 95
FT TURN 97 98
FT HELIX 100 109
FT TURN 113 115
SQ SEQUENCE 120 AA; 13443 MW; 6CA622DD3A4B27AD CRC64;

Query Match 40.0%; Score 201.5; DB 1; Length 120;
Best Local Similarity 38.7%; Pred. No. 5.2e-15;
Matches 43; Conservative 22; Mismatches 25; Indels 21; Gaps 4;

Qy 1 MKISVAIPIFFLLITIALGKTSS-----SRGP-----YH--PSBCCFTYT 40
Db 1 MKVSVAALSCMLVT-ALGSAQRTKDAETEFMMSKLPLENVLLDRFHATSADCCISYT 59

Qy 41 TYKIPRIMDYETNSQCSKPGIVFTIKRGHSVCTNPSPDKWQDYIKDMK 91
Db 60 PRSIPCSLLESYPETNSQCSKPGIVFTIKRGHSVCTNPSPDKWQDYIKDMK 110

RESULT 28
Q91265 ID Q91265 PRELIMINARY; PRT; 92 AA.
AC Q91265;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Macrophage inflammatory protein-1 alpha.
GN Name=MIP1 alpha;
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.

Query Match 39.1%; Score 197; DB 2; Length 88;
Best Local Similarity 40.4%; Pred. No. 1.2e-14;
Matches 40; Conservative 19; Mismatches 22; Indels 18; Gaps 3;

Qy 1 MKISVAIPIFFLLITIAL-----GKTESSSRGVHPHSECCFTYTYKIPRIMDYETNSQCS 60
Db 1 MKVPTAVLAVLLCI-ITLCNQVFSAPYGADTPTFCFSYGR-QIPKRFIADYFQTSLS 58

Qy 61 KPGIVFTIKRGHSVCTNPSPDKWQDYIKDMKEN 93
Db 59 EPGIIFUTKRRHVCADPKETWQVEIITDLELN 91

RESULT 29
Q8HYP8 ID Q8HYP8 PRELIMINARY; PRT; 88 AA.
AC Q8HYP8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chemokine CCL18/PARC.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciniae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22123042; PubMed=12126650; DOI=10.1006/cyto.2002.0875;
RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
RT "Molecular cloning and sequencing of 25 different rhesus macaque
RT chemokine cDNAs reveals evolutionary conservation among C, CC, CX,
RT AND CX3C families of chemokines.";
RL Cytokine 18:140-148(2002).
DR EMBL; AF449272; AAN76076.1; -.
DR HSP; P10147; IBS0.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR002473; C-X-C/interkn.8.
DR InterPro; IPR000827; CC_chemokine_sml.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 88 AA; 9797 MW; 19267D02F750D88F CRC64;

Query Match 39.1%; Score 197; DB 2; Length 88;
Best Local Similarity 40.4%; Pred. No. 1.2e-14;
Matches 40; Conservative 19; Mismatches 22; Indels 18; Gaps 3;

Qy 1 MKISVAIPIFFLLITIAL-----GKTESSSRGVHPHSECCFTYTYKIPRIMDYETNSQCS 60
Db 1 MKVPTAVLAVLLCI-ITLCNQVFSAPYGADTPTFCFSYGR-QIPKRFIADYFQTSLS 58

Qy 61 KPGIVFTIKRGHSVCTNPSPDKWQDYIKDMKEN 93
Db 59 EPGIIFUTKRRHVCADPKETWQVEIITDLELN 91
```

```
Db      1  MKGLAAL--LVLECTVALCSAQVTKKEP-----CCLVYTSRQIPQKFIVDYSE 48
Qy      55  TNSQCKPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93
Db      49  TSPQCTKPGVILLKRRRQICADPNKKWQYISDLKLN 87
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RESULT 30

```
SY05 RAT
ID -SY05 RAT      STANDARD;      PRT;      92 AA.
AC  P50231;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Small inducible cytokine A5 precursor (CCL5) (T-cell specific RANTES
DE  protein) (Sis-delta).
GN  Name=Ccl5; Synonyms=Scya5;
OS  Rattus norvegicus (Rat).
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
```

```
RP  SEQUENCE FROM N.A.
RC  STRAIN=Long Evans; TISSUE=Lung;
RA  Jones M.L., Shanley T.P., Ward P.A.;
RL  Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC  -!- FUNCTION: Chemoattractant for blood monocytes, memory T helper
CC  cells and eosinophils. Causes the release of histamine from
CC  basophils and activates eosinophils (By similarity).
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
```

```
CC  -----
DR  EMBL; U06436; AAA96499.1; -.
DR  HSSP; P13501; IRTN.
DR  RGD; 69069; Ccl5.
DR  InterPro; IPR000827; CC chemkine sml.
DR  InterPro; IPR001811; Chemokine_IL8.
DR  Pfam; PF00048; IL8; 1.
DR  SMART; SM00199; SCY; 1.
DR  PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW  Chemotaxis; Cytokine; Inflammatory response; Signal; T-cell.
FT  SIGNAL 1 24 Potential.
FT  CHAIN 25 92 Small inducible cytokine A5.
FT  DISULFID 34 58 By similarity.
FT  DISULFID 35 74 By similarity.
SQ  SEQUENCE 92 AA; 10170 MW; B4FBEC2B4208ABC6 CRC64;
```

```
Query Match      38.6%; Score 194.5; DB 1; Length 92;
Best Local Similarity 42.7%; Pred. No. 2.5e-14;
Matches 38; Conservative 15; Mismatches 31; Indels 5; Gaps 2;
```

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Qy      1  MKISVAAPFLIITLITGKTSSSRGPY--HPSECCFTYTYTKIPRQIMDYETNSQ 58
Db      1  MKISAAASLTIVLVAALCTVPAS---PYGSDTTPCCFAYLSIALPRAHVKEYFYTSSK 57
Qy      59  CSKPGIVFITKRGHSVCTNPSPDKWQDYI 87
Db      58  CSNLAVVFTVTRNRQVCANPEKKWQDYI 86
```

Search completed: September 19, 2005, 08:57:36
Job time : 177 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 19, 2005, 08:48:11 ; Search time 39 Seconds
(without alignments)
229.440 Million cell updates/sec

Title: US-10-626-530-2

Perfect score: 504

Sequence: 1 MKISVAIPFLITIALGT.....VCTNPDKWQDYIKDMKEN 93

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	240.5	47.7	93	2 B35673	LD78-beta protein
2	236	46.8	92	2 A30574	macrophage inflam
3	234.5	46.5	92	2 C30552	macrophage inflam
4	230.5	45.7	92	2 I46730	immune activation
5	224.5	44.5	92	1 A31767	macrophage inflam
6	223	44.2	92	2 A32393	macrophage inflam
7	223	44.2	92	2 I52322	macrophage inflam
8	191	37.9	91	1 A28815	monocyte chemoattr
9	189	37.5	91	1 A46539	monocyte chemoattr
10	183.5	36.4	120	2 J50177	lymphocyte and mon
11	180	35.7	116	2 I49555	gene C10 protein -
12	163	32.3	50	2 C60407	monocyte adherence
13	156	31.0	125	2 I46857	monocyte chemoattr
14	153.5	30.5	99	2 J42136	monocyte chemoattr
15	151	30.0	99	2 J5295	monocyte chemoattr
16	150.5	29.9	148	1 A30209	PDGF-inducible JF
17	149	29.6	148	1 S07723	immediate-early se
18	148.5	29.5	99	1 A39296	monocyte chemoattr
19	148.5	29.5	99	2 J42336	monocyte chemoattr
20	146	29.0	109	2 A54678	monocyte chemoattr
21	144	28.6	99	2 J42417	monocyte chemoattr
22	143	28.4	97	2 J41912	eotaxin precursor
23	135.5	26.9	96	2 J42478	eotaxin precursor
24	135.5	26.9	96	2 I48099	eotaxin precursor
25	127	25.2	99	2 A60299	monocyte chemoattr
26	126	25.0	120	2 I48147	monocyte chemoattr
27	123	24.4	95	2 A37236	I-309 protein prec
28	123	24.4	97	2 A48093	monocytic cytokine
29	122	24.2	72	2 A55984	monocyte chemoattr

30	116	23.0	114	1	ETHUL
31	93	18.5	114	1	ETMSL
32	86.5	17.2	92	2	S24236
33	85	16.9	101	2	I46871
34	82	16.3	101	2	S42496
35	81	16.1	103	2	A53096
36	79	15.7	95	2	JN0841
37	77.5	15.4	103	2	A26736
38	75.5	15.0	103	2	I50417
39	74	14.7	101	2	I48148
40	73	14.5	113	2	J47800
41	69	13.7	99	2	A37034
42	69	13.7	117	2	B44253
43	69	13.7	4488	1	RRHM2
44	68.5	13.6	311	2	T23873
45	68.5	13.6	316	2	H90372
46	67.5	13.4	1379	2	T13718
47	66.5	13.2	476	1	SGMSV
48	66	13.1	942	2	T19553
49	65.5	13.0	703	2	S08119
50	65.5	13.0	704	2	A26125
51	65	12.9	348	2	T03911
52	64	12.7	114	2	A55010
53	64	12.7	128	2	T15101
54	64	12.7	573	2	T49610
55	63.5	12.6	208	2	B83773
56	63.5	12.6	461	1	A35356
57	63	12.5	184	2	B72168
58	63	12.5	184	2	T28578
59	63	12.5	184	2	A36852
60	63	12.5	501	1	A60005
61	63	12.5	501	1	VBEMB
62	63	12.5	505	1	VBEMKH
63	62.5	12.4	496	2	T42562
64	62	12.3	100	2	I55614
65	62	12.3	100	2	S21467
66	62	12.3	107	2	JH0281
67	62	12.3	107	2	A28414
68	62	12.3	182	2	C90429
69	62	12.3	501	1	VBEMA
70	62	12.3	808	2	E64492
71	61.5	12.2	101	2	B28414
72	61.5	12.2	302	2	A70711
73	61.5	12.2	336	2	H69069
74	61.5	12.2	593	2	T20630
75	61.5	12.2	703	2	A44983
76	61	12.1	104	2	T30750
77	61	12.1	126	2	A35766
78	61	12.1	1732	2	T14039
79	60.5	12.0	164	2	C35216
80	60.5	12.0	207	2	S25990
81	60.5	12.0	234	2	AD0486
82	60.5	12.0	293	2	T09065
83	60.5	12.0	450	2	S15675
84	60.5	12.0	682	2	A35969
85	60	11.9	113	2	S06547
86	60	11.9	308	2	T29756
87	60	11.9	422	2	B31776
88	60	11.9	557	2	T22079
89	59.5	11.8	257	2	B81155
90	59.5	11.8	257	2	C81949
91	59.5	11.8	286	2	AD0523
92	59.5	11.8	311	2	T52312
93	59.5	11.8	347	2	T07108
94	59.5	11.8	411	2	T07806
95	59.5	11.8	527	2	F97197
96	59.5	11.8	611	2	G90542
97	59.5	11.8	702	2	C86268
98	59.5	11.8	934	2	T39941
99	59.5	11.8	982	2	S58881
100	59	11.7	90	2	S69133

lymphotactin precu
lymphotactin - mou
TCA3 protein - ra
interleukin-8 - ra
interleukin-8 prec
interleukin-8 prec
interleukin-8 - do
transformation-ind
RSV-induced protei
Neutrophil attract
neutrophil activat
interleukin-8 prec
alveolar macrophag
genome polyprotein
hypothetical prote
catechol 2,3-dioxy
pollux gene protei
vitronectin precu
hypothetical prote
heat shock protein
heat shock protein
r40cl protein - ri
neutrophil-activat
hypothetical prote
related to rna bin
hypothetical prote
tumor necrosis fac
A37R protein - var
8R protein - vario
A36R protein - var
glycoprotein A pre
glycoprotein A pre
glycoprotein gp57-
host shutoff virio
macrophage inflam
macrophage inflam
macrophage inflam
melanoma growth-st
hypothetical prote
hypothetical A pre
hypothetical prote
growth-regulated p
hypothetical prote
potassium channel
hypothetical prote
heat shock protein
chemokine homolog
platelet factor 4,
protein kinase (EC
FPI8 protein - low
hypothetical prote
probable exported
hypothetical prote
globulin-2 precurs
heparin-binding gr
finger protein (cl
hypothetical prote
hypothetical prote
conserved hypothet
hypothetical prote
spermidine synthas
deacetoxycephalosp
glucan endo-1,3-be
acyl-lacyl-carrier
uncharacterized co
gtp-binding protei
F13B4.2 protein -
hypothetical prote
mutS protein homol
platelet factor 4

RESULT 16

A30209 PDGF-inducible JE glycoprotein precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: A30209; A44771; A30861
R/Rollins, B.J.; Morrison, E.D.; Stiles, C.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 3738-3742, 1988
A/Title: Cloning and expression of JE, a gene inducible by platelet-derived growth factor
A/Reference number: A30209; MUID:88234501; PMID:3287374
A/Accession: A30209
A/Molecule type: DNA
A/Residues: 1-148 <ROL>
A/Cross-references: UNIPROT:P10148; GB:M19681; NID:g193486; PIDN:AAA37684.1; PID:g387168
R/Kawahara, R.S.; Deuel, T.F.
J. Biol. Chem. 264, 679-682, 1989
A/Title: Platelet-derived growth factor-inducible gene JE is a member of a family of smad
A/Reference number: A44771; MUID:89093129; PMID:2910858
A/Accession: A44771
A/Molecule type: DNA; mRNA
A/Residues: 1-148 <KA2>
A/Cross-references: GB:J04467; NID:g193488; PIDN:AAA37685.1; PID:g387169
C/Genetics:
A/Gene: JE
A/Introns: 26/1; 65/2
C/Superfamily: macrophage inflammatory protein
C/Keywords: cytokine; Glycoprotein
F/126/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	29.9%; Score 150.5; DB 1; Length 148;
Best Local Similarity	41.3%; Pred. No. 2.4e-09;
Matches	26; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

Qy 32 PSECCFTYTYKIPQRIMDYE-TNSQSKPGIVFKRGHGVCTNPSPDKWQDYIKOM 90
| | | | : | | | : | | | | : | | | | :
Db 31 PLTCCYSFTSKMIPMSRLSYKRIITSSRCPEAVVFTKLKREVCADPKKEWTYIKNL 90

Qy 91 KEN 93
|
Db 91 DRN 93

RESULT 17

S07723 Immediate-early serum-responsive protein JE precursor - rat
N/Alternate names: monocyte chemoattractant protein-1
C/Species: Rattus norvegicus (Norway rat)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: S07723; JN0128
R/Timmers, H.T.M.; Pronk, G.J.; Bos, J.L.; van der Eb, A.J.
Nucleic Acids Res. 18, 23-34, 1990
A/Title: Analysis of the rat JE gene promoter identifies an AP-1 binding site essential
A/Reference number: S07723; MUID:90174947; PMID:2106664
A/Accession: S07723
A/Molecule type: DNA
A/Residues: 1-148 <TIM>
A/Cross-references: UNIPROT:P14844; EMBL:X17053; NID:g55530; PIDN:CAA34901.1; PID:g55531
R/Yoshimura, T.; Takeya, M.; Takahashi, K.
Biochem. Biophys. Res. Commun. 174, 504-509, 1991
A/Title: Molecular cloning of rat monocyte chemoattractant protein-1 (MCP-1) and its exp
A/Reference number: JN0128; MUID:91128376; PMID:1704226
A/Accession: JN0128
A/Molecule type: mRNA
A/Residues: 1-148 <YOS>
A/Cross-references: GB:M57441; NID:g205333; PIDN:AAAG3496.1; PID:g205334
A/Experimental source: spleen cells
A/Note: the authors translated the codon GAA for residue 62 as Lys and GCT for residue 6
C/Genetics:
A/Introns: 26/1; 65/2
C/Superfamily: macrophage inflammatory protein
F/1-23/Domain: signal sequence #status predicted <SIG>
F/24-148/Product: immediate-early serum-responsive protein JE #status predicted <MAT>

C;Comment: This protein is identified as a potent eosinophil chemoattractant.

C;Superfamily: macrophage inflammatory protein

C;Keywords: Glycoprotein

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-96/Product: eotaxin #status predicted <MAT>

F;93/Binding site: carbohydrate (Thr) (covalent) #status predicted

Query Match 26.9%; Score 135.5; DB 2; Length 96;
Best Local Similarity 37.2%; Pred. No. 7.3e-08;
Matches 32; Conservative 11; Mismatches 38; Indels 5; Gaps 2;

Qy 1 MKISVAIPIPELLITIALGKTESSRGYPHPSCCFYTYTKIPQRIWDY-YETNSQC 59

Db 1 MKVSTA----FLCLLLTVSAFSAQVLAHGIPSCCFRVTKKLSFORLSKYKIITSSKC 56

Qy 60 SKPGIVFTRKGHSVCTNPNSDKWQD 85

Db 57 PQTAIVEIPIKDKMICADPKKKWQD 82

RESULT 24

I48099

eotaxin precursor - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I48099

R;Rothenberg, M.E.; Luster, A.D.; Lilly, C.M.; Drazen, J.M.; Leder, P.

J. Exp. Med. 181, 1211-1216, 1995

A;Title: Constitutive and allergen-induced expression of eotaxin mRNA in the guinea pig

A;Reference number: I48099; MUID:95173589; PMID:7869037

A;Accession: I48099

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-96 <RES>

A;Cross-references: UNIPROT:P80325; EMBL:U18941; NID:5687655; PIDN:AAC52180.1; PID:56876

C;Superfamily: macrophage inflammatory protein

Query Match 26.9%; Score 135.5; DB 2; Length 96;
Best Local Similarity 37.2%; Pred. No. 7.3e-08;
Matches 32; Conservative 11; Mismatches 38; Indels 5; Gaps 2;

Qy 1 MKISVAIPIPELLITIALGKTESSRGYPHPSCCFYTYTKIPQRIWDY-YETNSQC 59

Db 1 MKVSTA----FLCLLLTVSAFSAQVLAHGIPSCCFRVTKKLSFORLSKYKIITSSKC 56

Qy 60 SKPGIVFTRKGHSVCTNPNSDKWQD 85

Db 57 PQTAIVEIPIKDKMICADPKKKWQD 82

RESULT 25

A60299

monocyte chemoattractant protein 1 precursor - human

N;Alternate names: GDCP-1; glioma-derived monocyte chemotactic factor 1; MCAF; MCP-1; monocyte chemoattractant protein 1; glioma-derived chemotactic factor 2 (GDCP-2)

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 09-Jul-2004

C;Accession: A35474; A33476; S03339; I51841; A60299; A32396; A34561; I57488; JCI

R;Shyy, Y.J.; Li, Y.S.; Kolattukudy, P.E.

Biochem. Biophys. Res. Commun. 169, 346-351, 1990

A;Title: Structure of human monocyte chemotactic protein gene and its regulation by TPA.

A;Reference number: A35474; MUID:90290466; PMID:2357211

A;Accession: A35474

A;Molecule type: DNA

A;Residues: 1-99 <SHV>

A;Cross-references: UNIPROT:P13500; GB:M37719; NID:5187447; PIDN:AAA18102.1; PID:5487124

R;Rollins, B.J.; Stier, P.; Ernst, T.; Wong, G.G.

Mol. Cell. Biol. 9, 4687-4695, 1989

A;Title: The human homolog of the JE gene encodes a monocyte secretory protein.

A;Reference number: A33476; MUID:90097880; PMID:2513477

A;Accession: A33476

A;Molecule type: mRNA

A;Residues: 1-99 <ROL>

A;Cross-references: GB:M30816; GB:M31625; GB:M31626; NID:5188701; PIDN:AAA36330.1; PID:5188701; Yoshimura, T.; Yuhki, N.; Moore, S.K.; Appella, E.; Lerman, M.I.; Leonard, E.J. FEBS Lett. 244, 487-493, 1989

A;Title: Human monocyte chemoattractant protein-1 (MCP-1). Full-length cDNA cloning, expression, and characterization of the protein.

A;Reference number: S03339; MUID:89153605; PMID:2465924

A;Accession: S03339

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-99 <YOS>

A;Cross-references: GB:X14768; NID:934513; PIDN:CAA32876.1; PID:934514

A;Experimental source: glioma cell line U-105MG

R;Yoshimura, T.; Leonard, E.J.

Adv. Exp. Med. Biol. 305, 47-56, 1991

A;Title: Human monocyte chemoattractant protein-1 (MCP-1).

A;Reference number: I51841; MUID:92095166; PMID:1661560

A;Accession: I51841

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-99 <YOS>

A;Cross-references: GB:S71513; NID:9240867; PIDN:AAB20651.1; PID:9240868

R;Bottazzi, B.; Colotta, F.; Sica, A.; Nobili, N.; Mantovani, A.

Int. J. Cancer 45, 795-797, 1990

A;Title: A chemoattractant expressed in human sarcoma cells (tumor-derived chemotactic factor-1/MCAF).

A;Reference number: A60299; MUID:90216082; PMID:2182547

A;Accession: A60299

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-99 <BOT>

R;Puttani, Y.; Nomura, H.; Notsake, M.; Oyama, Y.; Fukui, T.; Yamada, M.; Larsen, C.G.; Biochem. Biophys. Res. Commun. 159, 249-255, 1989

A;Title: Cloning and sequencing of the cDNA for human monocyte chemotactic and activating factor (MCAF).

A;Reference number: A32300; MUID:89165862; PMID:2923622

A;Accession: A32300

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-99 <FUR>

A;Cross-references: GB:M24545; NID:9187434; PIDN:AAA18164.1; PID:9307163

R;Robinson, E.A.; Yoshimura, T.; Leonard, E.J.; Tanaka, S.; Griffin, P.R.; Shabanowitz, S. Proc. Natl. Acad. Sci. U.S.A. 86, 1850-1854, 1989

A;Title: Complete amino acid sequence of a human monocyte chemoattractant, a putative monocyte chemoattractant protein-1 (MCP-1).

A;Reference number: A32396; MUID:89184525; PMID:2648385

A;Accession: A32396

A;Molecule type: protein

A;Residues: 'X', 25-99 <ROB>

R;Decock, B.; Conings, R.; Lenaerts, J.P.; Billiau, A.; Van Damme, J.

Biochem. Biophys. Res. Commun. 167, 904-909, 1990

A;Title: Identification of the monocyte chemotactic protein from human osteosarcoma cells.

A;Reference number: A34561; MUID:90211336; PMID:2322286

A;Accession: A34561

A;Molecule type: protein

A;Residues: 29-33, 'XX', 36-52:82-92 <DEC>

R;Li, Y.S.; Shyy, Y.J.; Wright, J.G.; Valente, A.J.; Cornhill, J.F.; Kolattukudy, P.E. Mol. Cell. Biochem. 126, 61-68, 1993

A;Title: The expression of monocyte chemotactic protein (MCP-1) in human vascular endothelial cells.

A;Reference number: I57488; MUID:94150478; PMID:8107690

A;Accession: I57488

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-99 <LIY>

A;Cross-references: GB:S69738; NID:9545464; PIDN:AAB29926.1; PID:9545465

R;Ye, Q.N.; Su, G.F.; Yuan, Y.; Huang, C.F.

Chinese J. Microbiol. Immunol. 14, 29-32, 1994

A;Title: The PCR cloning and sequencing of human monocyte chemoattractant protein-1 (MCP-1).

A;Reference number: JCI096

A;Accession: JCI096

A;Molecule type: mRNA

A;Residues: 24-28, 'Q', 30-99 <YEQ>

C;Genetics:

A;Gene: GDB:SCYA2

A;Cross-references: GDB:125279; OMIM:158105

A;Map position: 17q11.2-17q12

A55984

monocyte chemotactic protein bo-MCP-lb - bovine (fragments)

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 09-May-1997

C;Accession: A55984

R;Proost, P.; Wuyts, A.; Lenaerts, J.P.; Van Damme, J.

Biochemistry 33, 13406-13412, 1994

A;Title: Purification, sequence analysis, and biological characterization of a second bovine monocyte chemotactic protein

A;Reference number: A55984; MUID:95034774; PMID:7947749

A;Accession: A55984

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-72 <PRO>

C;Superfamily: macrophage inflammatory protein

Query Match 24.2%; Score 122; DB 2; Length 72;
Best Local Similarity 42.2%; Pred. No. 1.7e-06;
Matches 27; Conservative 10; Mismatches 23; Indels 4; Gaps 3;

Qy 32 PSECFTYTYKIPRIMDYIE-TNSQCSKPGIVFTKRGHSVCTNPSPDKWQDYIKDM 90

Db 6 PVTCCYLTGKISMORLSYRRVTSSKCPKPAVIFKTIAGKEIXAEP--KWQDSISHL 63

Qy 91 -KEN 93

Db 64 DKKN 67

RESULT 30

ETHUL

Lymphotactin precursor - human

N;Alternate names: activation-induced chemokine-related protein (ATAC); single cysteine

N;Contains: eosinophilic peptide

C;Species: Homo sapiens (man)

C;Date: 23-Oct-1981 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004

C;Accession: S60650; I38978; A03190; I53506

R;Mueller, S.; Dörner, B.; Korthauer, U.; Mages, H.W.; D'Apuzzo, M.; Senger, G.; Kroese

Eur. J. Immunol. 25, 1744-1748, 1995

A;Title: Cloning of ATAC, an activation-induced, chemokine-related molecule exclusively

A;Reference number: S60650; MUID:95339892; PMID:7615002

A;Accession: S60650

A;Molecule type: mRNA

A;Residues: 1-114 <MUE>

A;Cross-references: UNIPROT:P47992; EMBL:X86474; NID:9895846; PIDN:CAA60198.1; PID:98958

R;Kennedy, J.; Kellner, G.S.; Kleyensteuber, S.; Schall, T.J.; Weiss, M.C.; Yssel, H.; Sc

J. Immunol. 155, 203-209, 1995

A;Title: Molecular cloning and functional characterization of human lymphotactin.

A;Reference number: I38978; MUID:95325590; PMID:7602097

A;Accession: I38978

A;Status: translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-114 <KEN>

A;Cross-references: EMBL:U23772; NID:g902001; PIDN:AAC50164.1; PID:g902002

R;Goettl, E.J.; Austen, K.F.

Proc. Natl. Acad. Sci. U.S.A. 72, 4123-4127, 1975

A;Title: Purification and synthesis of eosinophilic tetrapeptides of human lung tis

A;Reference number: A03190; MUID:76078412; PMID:1060093

A;Accession: A03190

A;Molecule type: protein

A;Residues: 22-25 <GOE>

A;Note: 22-Ala was also seen

R;Yoshida, T.; Imai, T.; Kakizaki, M.; Nishimura, M.; Yoshie, O.

FEBS Lett. 360, 155-159, 1995

A;Title: Molecular cloning of a novel C or gamma type chemokine, SCW-1.

A;Reference number: I53506; MUID:95180438; PMID:7875320

A;Accession: I53506

A;Status: translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-114 <YOS>

A;Cross-references: GB:D43768; NID:g927650; PIDN:BAA07825.1; PID:g927651

C;Comment: Lymphotactin is produced by activated T-cells and is chemotactic for some lym

C;Comment: Eosinophilic peptide is released from mast cells in lung and other tissu

ially affecting eosinophils, include chemotaxis, chemotactic deactivation, release of en

C;Comment: It has not yet been shown that the previously detected eosinophilotactic pepti

C;Genetics:

A;Gene: GDB:SCYC1; LTN; LPTN; ATAC

A;Cross-references: GDB:682094

A;Map position: 1q23-1q25

C;Superfamily: lymphotactin

C;Keywords: chemotaxis; cytokine; lymphokine; mast cell; T-cell

F;1-15/Domain: signal sequence #status predicted <SIG>

F;16-21/Domain: propeptide #status predicted <PRO>

F;22-114/Product: lymphotactin #status predicted <MAT>

F;22-25/Product: eosinophilotactic peptide #status predicted <EOP>

F;32-69/Disulfide bonds: #status predicted

Query Match 23.0%; Score 116; DB 1; Length 114;

Best Local Similarity 31.5%; Pred. No. 1.2e-05;

Matches 29; Conservative 18; Mismatches 35; Indels 10; Gaps 3;

Qy 1 MKISVAIIPFLIIT--IALGTXTSSSRGYPHPSCCFTYTYKIPRQIMDYETNSQ 58

Db 1 MRLLIALLIGICSLTAYIVEGVGSEVSDK-----RTCVSLTTQRLPVSRIKTY--TITE 52

Qy 59 CSKPGIVFITKRGHSVCTNPSPDKWQDYIKDM 90

Db 53 GSLRAVIFITKRGCLKYCADPQATWVRDVRSM 84

Search completed: September 19, 2005, 08:58:21

Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 19, 2005, 08:44:26 ; Search time 165 Seconds
(without alignments)
217.992 Million cell updates/sec

Title: US-10-626-530-2

Perfect score: 504

Sequence: 1 MKTSVAIPFLIITLALGT.....VCTNPSDKWQDYIKDMKEN 93

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq_16Dec04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	504	100.0	93	2	AAR76128 Macrophag
2	504	100.0	93	2	AAR95691 Pituitary
3	504	100.0	93	2	AAW07203 Human MIP
4	504	100.0	93	2	AAW38171 Human che
5	504	100.0	93	2	AAW57697 Human M-C
6	504	100.0	93	3	AAB27659 Human pro
7	504	100.0	93	3	AAB15806 Human che
8	504	100.0	93	4	AAB68294 Amino aci
9	504	100.0	93	4	AAB50992 Human PRO
10	504	100.0	93	5	ABB90773 Human Tum
11	504	100.0	93	5	ABB90774 Human Tum
12	504	100.0	93	5	ABB90772 Human Tum
13	504	100.0	93	6	ABU61834 Chemokine
14	504	100.0	93	6	ABU61832 Human MIP
15	504	100.0	93	6	ABU61833 Pituitary
16	504	100.0	93	6	ABU54479 Human nor
17	504	100.0	93	6	ABU54481 Human nor
18	504	100.0	93	6	ABU54480 Human nor
19	504	100.0	93	6	ABP76018 Human GEN
20	504	100.0	93	7	ADD06466 Human Ckb
21	504	100.0	93	7	ADP15213 Human alb
22	504	100.0	93	7	ADP16716 Human alb
23	504	100.0	93	7	ADP16713 Human alb
24	504	100.0	93	7	ADP16715 Human alb
25	504	100.0	93	7	ADP15205 Human alb

26	504	100.0	93	7	ADF15332 Human alb
27	504	100.0	93	7	ADF16667 Human alb
28	504	100.0	93	7	ADF16714 Human alb
29	504	100.0	93	7	ADF16739 Human alb
30	504	100.0	93	7	ADF15204 Human alb
31	504	100.0	93	7	ADF15208 Human alb
32	504	100.0	93	7	ADF15209 Human alb
33	504	100.0	93	7	ADF15224 Human alb
34	504	100.0	93	7	ADF15309 Human alb
35	504	100.0	93	7	ADF15326 Human alb
36	504	100.0	93	7	ADF16712 Human alb
37	504	100.0	93	7	ADF16686 Human alb
38	504	100.0	93	7	ADF16694 Human alb
39	504	100.0	143	6	ABU61831 Macrophag
40	482	95.6	109	2	AAW38172 Human che
41	482	95.6	109	2	AAW82723 Human CCC
42	482	95.6	109	8	ADN04138 Antipsoxi
43	480	95.2	88	2	AAW52843 Human mat
44	416	82.5	74	2	AAR77600 Human cir
45	416	82.5	74	4	AAB68295 Amino aci
46	416	82.5	74	5	AAO20020 Human che
47	416	82.5	74	5	AAO14153 Human HCC
48	416	82.5	74	5	AAO21107 HCC1 chem
49	416	82.5	74	5	AAO21097 Protein o
50	416	82.5	74	7	ADF16638 Human alb
51	416	82.5	74	7	ADF16641 Human alb
52	416	82.5	74	7	ADF16640 Human alb
53	416	82.5	74	7	ADF16636 Human alb
54	416	82.5	74	7	ADF16637 Human alb
55	416	82.5	74	7	ADF16634 Human alb
56	416	82.5	74	7	ADF16642 Human alb
57	416	82.5	74	7	ADF16635 Human alb
58	416	82.5	74	7	ADF16633 Human alb
59	416	82.5	74	7	ADF16639 Human alb
60	416	82.5	660	7	ADD06557 Human Ckb
61	416	82.5	660	7	ADD06554 Human Ckb
62	416	82.5	683	7	ADF14991 Human alb
63	416	82.5	683	7	ADF14990 Human alb
64	416	82.5	684	7	ADD06556 Human Ckb
65	416	82.5	1184	7	ADD06553 Human Ckb
66	415	82.3	87	7	ADD06550 Human Ckb
67	415	82.3	672	7	ADF16479 Human alb
68	413	81.9	74	2	AAR76545 Human cir
69	411	81.5	681	7	ADF16471 Human alb
70	411	81.5	682	7	ADF16470 Human alb
71	405	80.4	680	7	ADD06587 Human Ckb
72	405	80.4	680	7	ADF16472 Human alb
73	402	79.8	673	7	ADF16550 Human alb
74	401	79.6	656	7	ADD06594 Human Ckb
75	400.5	79.5	736	7	ADF15095 Human alb
76	399	79.2	72	2	AAW17659 Stem cell
77	399	79.2	72	6	ABU61830 Human che
78	399	79.2	677	7	ADD06589 Human Ckb
79	399	79.2	677	7	ADF16475 Human alb
80	398	79.0	679	7	ADF16473 Human alb
81	396.5	78.7	673	7	ADF16551 Human alb
82	393.5	78.1	678	7	ADF16474 Human alb
83	392	77.8	69	7	ADE80853 HCC1 chem
84	392	77.8	671	7	ADF16539 Human alb
85	391.5	77.7	672	7	ADF16549 Human alb
86	388	77.0	653	7	ADD06595 Human Ckb
87	386	76.6	94	4	AAO11593 Human pol
88	386	76.6	94	7	ADE08943 Novel pro
89	386	76.6	671	7	ADF16552 Human alb
90	386	76.6	692	7	ADD06565 Human Ckb
91	385.5	76.5	676	7	ADD06591 Human Ckb
92	385.5	76.5	676	7	ADD06593 Human Ckb
93	385.5	76.5	676	7	ADF16476 Human alb
94	385.5	76.5	680	7	ADF16557 Human alb
95	385	76.4	115	8	ADQ66457 Novel hum
96	385	76.4	675	7	ADF14994 Human alb
97	385	76.4	675	7	ADF14995 Human alb
98	385	76.4	676	7	ADD06559 Human Ckb

99 385 76.4 676 7 ADD06562 Human Ckb
100 385 76.4 691 7 ADF14999 Human alb

ALIGNMENTS

RESULT 1

AAR76128
ID AAR76128 standard; protein; 93 AA.

XX AC AAR76128;
XX 25-MAR-2003 (revised)
DT 02-DEC-1995 (first entry)
XX Macrophage inflammatory protein-1-gamma.
DE Macrophage inflammatory protein-1-gamma; therapeutic; diagnostic.
XX Homo sapiens.

XX FH Key Location/Qualifiers
FT Peptide 1..24
FT /note= "signal peptide"
XX W09517092-A1.
XX 29-JUN-1995.
XX 28-JUN-1994; 94WO-US007256.
XX 22-DEC-1993; 93US-00173209.
PR 08-MAR-1994; 94US-00208339.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Li H, Rosen CA, Ruben S, Adams MD;
XX WPI; 1995-240404/31.
DR N-PSDB; AAQ94094.

XX cDNA encoding human macrophage inflammatory proteins -3, -4 and -1 gamma
PT - used in immuno-regulation including inflammatory activity,
PT haematopoiesis, treatment of psoriasis or solid tumours.
XX Claim 48; Fig 8; 60pp; English.
XX Human macrophage inflammatory protein-1-gamma (MIP-1g) is used in
CC therapeutic and diagnostic applications for detecting and treating
CC infections, cancer, inflammation, myelopietic dysfunction and autoimmune
CC diseases. Antagonists/inhibitors of MIP-1g are used to treat diseases
CC involving overexpression of MIP-1g, including silicosis,
CC arteriosclerosis, autoimmune and chronic inflammatory and infective
CC diseases, aplastic anaemia, etc. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX Sequence 93 AA;

Query Match 100.0%; Score 504; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-52;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKISVAAIPFLLITLITLALGKTSSSRGYPHPSECCFTYTYKIPQRIMDYETNSQCS 60
DB 1 MKISVAAIPFLLITLITLALGKTSSSRGYPHPSECCFTYTYKIPQRIMDYETNSQCS 60

QY 61 KPGIVFTKRGHVSCTNPSPDKWQDYIKDMKEN 93
DB 61 KPGIVFTKRGHVSCTNPSPDKWQDYIKDMKEN 93

RESULT 2

AAR95691
ID AAR95691 standard; protein; 93 AA.

XX AC AAR95691;
XX 20-DEC-1996 (first entry)
XX Pituitary expressed chemokine (PGECC).

XX Chemokine; liver; pituitary gland; LVEC; PGECC; inflammation; detection;
KW identification; MCP receptor; CC-CKR1 receptor.
XX Homo sapiens.
XX W09616979-A1.
XX 06-JUN-1996.
XX 29-NOV-1995; 95WO-US015484.
PR 29-NOV-1994; 94US-00347492.
XX (INCY-) INCYTE PHARM INC.
XX Wilde CG, Hawkins PR, Bandman O, Seilhamer JU, Neote KS;
XX WPI; 1996-277714/28.
DR N-PSDB; AAT31762.

XX Liver and pituitary gland expressed chemokine(s) - useful for diagnosis
PT of inflammation.
XX Claim 1; Fig 7; 48pp; English.

XX The nucleotide sequences encoding liver or pituitary expressed chemokines
CC (LVEC or PGECC - See AAT31760-62) or primers derived from them, may be
CC used for the detection of LVEC/PGECC encoding sequences in a biological
CC sample. The presence of abnormal levels of the nucleotide sequences
CC encoding LVEC's correlates highly with inflammation of the liver. The
CC PGECC is used to selectively affect the CC-CKR1 receptor over the MCP
CC receptor
XX Sequence 93 AA;

Query Match 100.0%; Score 504; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-52;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKISVAAIPFLLITLITLALGKTSSSRGYPHPSECCFTYTYKIPQRIMDYETNSQCS 60
DB 1 MKISVAAIPFLLITLITLALGKTSSSRGYPHPSECCFTYTYKIPQRIMDYETNSQCS 60

QY 61 KPGIVFTKRGHVSCTNPSPDKWQDYIKDMKEN 93
DB 61 KPGIVFTKRGHVSCTNPSPDKWQDYIKDMKEN 93

RESULT 3
AAW07203

ID AAW07203 standard; protein; 93 AA.

XX AC AAW07203;
XX 02-JUL-1997 (first entry)
XX Human MIP-4: a chemoattractant for leukocytes.

XX Leukocyte; attractant; affinity; leukaemia; immunity; wound healing;
KW diagnosis; drug screening; inflammation; haematopoiesis regulator;
KW psoriasis; stroke; thrombocytosis; pulmonary embolism; asthma; arthritis;
KW aplastic anaemia; endotoxemic shock; MIP; macrophage inflammatory protein.

XX Homo sapiens.

```

XX FH Key Location/Qualifiers
XX FT Peptide 1..19
XX FT /label= sig_peptide
XX FT Protein 20..93
XX FT /label= mat_protein
XX XX
XX FN WO9634891-A1.
XX XX
XX PD 07-NOV-1996.
XX XX
XX PF 23-JUN-1995; .95WO-US009058.
XX XX
XX PR 05-MAY-1995; .95US-00446881.
XX XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX XX
XX PI Rosen CA, Ruben SM, Li H, Adams MD;
XX XX
XX DR WPI; 1996-506106/50.
XX DR N-PSDB; AAT44362.
XX XX
XX PT New nucleic acid encoding the new human chemokine beta-8 - with
XX FT chemoattractant activity for leucocytes, for treating leukaemia,
XX FT stimulating immunity and wound healing, also for diagnosis and drug
XX FT screening.
XX XX
XX PS Example 2; Page 58; 93pp; English.
XX XX
XX CC Human macrophage inflammatory protein-4 (MIP-4) is an attractant for
XX CC leucocytes and is involved in the regulation of immune responses and
XX CC inflammation, e.g. stimulating synthesis of other cytokines. DNA encoding
XX CC MIP-4, MIP-4, and agonists of MIP-4 are useful for protecting bone marrow
XX CC against chemotherapeutic agents, for eliminating leukaemia cells (by
XX CC inducing apoptosis), stimulating an immune response and regulating
XX CC haematopoiesis (inhibiting proliferation and differentiation of cells)
XX CC and lymphocyte trafficking. MIP-4 is also used to treat psoriasis and
XX CC solid tumours; to increase host defences against chronic and acute
XX CC infection and to stimulate wound healing. MIP-4 also increase vascular
XX CC permeability, and can be used to treat stroke, thrombocytosis, pulmonary
XX CC embolism and myeloproliferative disease, and for identification of
XX CC specific receptors. Antagonists of MIP-4 are used to inhibit the
XX CC production of IL-1 and TNF-alpha and to treat e.g. aplastic anaemia,
XX CC myelodysplastic syndrome, asthma, arthritis (and many other autoimmune
XX CC and inflammatory diseases), infections, endotoxic shock, atherosclerosis,
XX CC allergy etc. MIP-4 and DNA encoding it may also be used in drug
XX CC development
XX XX
XX SQ Sequence 93 AA;
XX XX
XX Query Match 100.0%; Score 504; DB 2; Length 93;
XX Best Local Similarity 100.0%; Pred. No. 1e-52;
XX Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 MKISVAIIPFLITIALGTTKTSRSSRGYPHPSECCFTYTYKIPRORIMDYETNSQCS 60
XX Db 1 MKISVAIIPFLITIALGTTKTSRSSRGYPHPSECCFTYTYKIPRORIMDYETNSQCS 60
XX
XX Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93
XX Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93
XX
XX RESULT 5
XX AAW57697
XX ID AAW57697 standard; protein; 93 AA.
XX AC AAW57697;
XX XX
XX DT 13-OCT-1998 (first entry)
XX DE Human M-CIF protein.
XX XX
XX KW Monocyte colony inhibitory factor; M-CIF; therapy; proliferation;
XX KW differentiation; low proliferative potential-colony forming cell;
XX KW colony forming unit-granulocyte; monocyte; chemotherapy; radiation;

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XX Tandem gene; chemokine CC-2; chemokine CC-3; chemokine HCC-1; human;
XX KW cell migration; immune system.
XX OS Homo sapiens.
XX PN WO9741230-A2.
XX PD 06-NOV-1997.
XX PF 30-APR-1997; .97WO-EP002217.
XX PR 30-APR-1996; .96DE-01017312.
XX PA (FORS/) FORSSMANN W.
XX XX
XX PI Forssmann W, Pardigol A, Maegert H, Schulz-Knappe P;
XX XX
XX DR WPI; 1997-549733/50.
XX DR N-PSDB; AAT95743.
XX XX
XX PT New nucleic acid of tandem human gene for chemokines CC-2 and CC-3 - used
XX FT for treating disorders of cell migration, the immune system and growth
XX FT functions.
XX XX
XX PS Claim 1; Page 16; 19pp; German.
XX XX
XX CC Novel nucleic acids of a tandem gene contain AAT95743 or AAT95744 and
XX CC encode the human chemokines CC-2 and CC-3. Transcription of the tandem
XX CC gene generates a bicistronic mature RNA containing two non-overlapping
XX CC open reading frames (ORF). AAT95743 has a 1st ORF for AAW38170, i.e. CC-
XX CC 2, and a 2nd ORF for AAW38171, i.e. the known chemokine HCC-1. AAT95744,
XX CC formed by alternative splicing of the primary transcript, has the same
XX CC 1st ORF but the 2nd encodes AAW38172, a variant form of HCC-1 having a 16
XX CC amino acid insertion, i.e. CC-3. The tandem gene has two functional
XX CC promoter regions, suggesting independent expression of the ORF. cDNA for
XX CC the bicistron was produced from the total RNA of T84 cells by 5'-rapid
XX CC amplification of complementary ends (RACE). The gene corresponding to
XX CC this DNA was isolated on chromosome 17, and found to have seven exons,
XX CC four for CC-2 and three for HCC-1/CC-3, separated by about 12 kb. CC-2
XX CC and CC-3 can be used to treat disorders of cell migration, the immune
XX CC system and growth functions. Also antibodies against them, and fragments
XX CC that hybridise to the cDNA, can be used for diagnosis. (Updated on 25-MAR
XX CC -2003 to correct PR field.)
XX XX
XX SQ Sequence 93 AA;
XX XX
XX Query Match 100.0%; Score 504; DB 2; Length 93;
XX Best Local Similarity 100.0%; Pred. No. 1e-52;
XX Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 MKISVAIIPFLITIALGTTKTSRSSRGYPHPSECCFTYTYKIPRORIMDYETNSQCS 60
XX Db 1 MKISVAIIPFLITIALGTTKTSRSSRGYPHPSECCFTYTYKIPRORIMDYETNSQCS 60
XX
XX Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93
XX Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93
XX
XX RESULT 5
XX AAW57697
XX ID AAW57697 standard; protein; 93 AA.
XX AC AAW57697;
XX XX
XX DT 13-OCT-1998 (first entry)
XX DE Human M-CIF protein.
XX XX
XX KW Monocyte colony inhibitory factor; M-CIF; therapy; proliferation;
XX KW differentiation; low proliferative potential-colony forming cell;
XX KW colony forming unit-granulocyte; monocyte; chemotherapy; radiation;

```

KW myeloproliferative disorder; suppressor; inhibitor.
OS Homo sapiens.
XX WO9814592-A1.
XX 09-APR-1998.
XX
XX 30-SEP-1997; 97WO-US017505.
XX
PR 30-SEP-1996; 96US-0027299P.
PR 30-SEP-1996; 96US-0027300P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Gentz RL, Patel V, Kreider BL, Zhang J, Antonaccio M, Mendrick D;
PI Jimenez P;
XX
XX WPI; 1998-240087/21.
DR N-PSDB; AAV24501.
XX
XX Inhibiting proliferation or differentiation of myeloid progenitor cells -
PT using myeloid progenitor inhibitory factor-1 amino-terminal deletion
PT mutant.
XX
PS Claim 79; Page 178; 298pp; English.
XX
CC This sequence represents a monocyte colony inhibitory factor (M-CIF)
CC which is used in a method for inhibiting proliferation or differentiation
CC of myeloid progenitor cells, specifically low proliferative potential-
CC colony forming cells or colony forming unit-granulocyte and monocyte
CC cells, in an human individual undergoing therapy that kills dividing
CC cells, especially chemotherapy or radiation therapy, where the
CC polypeptide results in accelerated recovery of platelets or granulocytes
CC alleviating thrombocytopenia or neutropenia. The polypeptide can be
CC administered to treat a myeloproliferative disorder, especially essential
CC thrombocyctosis, polycythemia vera and agnogenic myeloid metaplasia. The
CC polypeptide can also be used for myeloprotection, to inhibit growth of
CC hematopoietic progenitor cells, to treat sepsis, to suppress TNF-alpha
CC production, to treat renal injury, arthritis or joint inflammation,
CC enterocolitis or lupus
XX
SQ Sequence 93 AA;

Query Match 100.0%; Score 504; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-52; Indels 0; Gaps 0;
Matches 93; Conservative 0; Mismatches 0;

QY 1 MKISVAAIPFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60
DB 1 MKISVAAIPFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60

QY 61 KPGIVFTTKRGHSVCTNPSPDKWQDYIKDMKEN 93
DB 61 KPGIVFTTKRGHSVCTNPSPDKWQDYIKDMKEN 93

RESULT 6
AAB27659
ID AAB27659 standard; protein; 93 AA.
XX
XX AAB27659;
XX
DT 26-JAN-2001 (first entry)
XX
DE Human protein PRO877.
XX
KW Cardiovascular; endothelial; angiogenic disorder; PRO179; PRO238; PRO364;
KW PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333; PRO840; PRO877; PRO878;
KW PRO879; PRO882; PRO885; PRO887; gene therapy.
XX
OS Homo sapiens.
XX

PH Key Location/Qualifiers
FT Peptide 1..22
FT /label= Signal peptide
XX
PN WO200053757-A2.
XX
PD 14-SEP-2000.
XX
XX 24-FEB-2000; 2000WO-US005004.
XX
XX 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 02-JUN-1999; 99WO-US012252.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028409.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;
PI Goddard A, Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pitti RM;
PI Watanabe CK, Williams PM, Wood WI;
XX
XX WPI; 2000-611444/58.
DR N-PSDB; AAA99911.
XX
XX Novel PRO polypeptides and agonists and antagonists of them, used to
PT diagnose and treat cardiovascular, endothelial and angiogenic disorders.
XX
XX Claim 71; Fig 22; 181pp; English.
XX
CC The present invention relates to methods for stimulating or inhibiting
CC angiogenesis and cardiovascularization. The methods involve the use of
CC pharmaceutical compositions based on the following proteins, PRO179,
CC PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333, PRO840,
CC PRO877, PRO878, PRO882, PRO885 or PRO887. These proteins were
CC identified by isolating cDNA clones encoding secreted proteins. The
CC proteins of the invention may be used to diagnose and treat
CC cardiovascular, endothelial or angiogenic disorders. The present sequence
CC is one of the proteins of the invention
XX
SQ Sequence 93 AA;

Query Match 100.0%; Score 504; DB 3; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-52; Indels 0; Gaps 0;
Matches 93; Conservative 0; Mismatches 0;

QY 1 MKISVAAIPFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60
DB 1 MKISVAAIPFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60

QY 61 KPGIVFTTKRGHSVCTNPSPDKWQDYIKDMKEN 93
DB 61 KPGIVFTTKRGHSVCTNPSPDKWQDYIKDMKEN 93

RESULT 7
AAB15806
ID AAB15806 standard; protein; 93 AA.
XX
XX AAB15806;
XX
DT 17-JAN-2001 (first entry)
XX
DE Human chemokine HCC-1 SEQ ID NO: 48.

XX Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;
 KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;
 KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;
 KW basophil-mediated disease; myocardial infarction; acute ischaemia;
 KW rheumatoid arthritis; contraception.
 XX
 OS Homo sapiens.
 XX
 XX WO200042071-A2.
 XX
 XX 20-JUL-2000.
 XX
 XX 12-JAN-2000; 2000WO-US000821.
 XX
 XX 12-JAN-1999; 99US-00229071.
 XX
 XX 17-MAR-1999; 99US-00271192.
 XX
 XX 01-DEC-1999; 99US-00452406.
 XX
 XX (NBOR-) NBORX CORP.
 XX
 XX Grainger DJ, . Tatalick LM;
 XX
 XX WPI: 2000-499101/44.
 XX
 XX N-PSDB; AAA74875.
 XX
 XX New peptide 3, amide and heterocyclic compounds and saccharide conjugates
 PT used for inhibiting chemokine induced activity and for treating e.g.
 PT stroke, vascular diseases, autoimmune diseases and tumor growth.
 XX
 XX Disclosure; Page 360-361; 387pp; English.
 XX
 XX The present invention concerns the identification of a number of
 CC chemokines which can be used to produce derivatives, agonists and
 CC antagonists which are then useful in disease treatment. The chemokines
 CC include sequences AB15785-B15794, AB15803-B15813 and AB15831-B15848.
 CC These chemokine derivatives can be used to treat diseases such as
 CC autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and
 CC AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated
 CC diseases, endotoxaemia, myocardial infarction, acute ischaemia and
 CC rheumatoid arthritis, and can be used to prevent strokes and as
 CC contraceptives. The coding sequences for the chemokines can be used in
 CC gene therapy for the same diseases, as well as in the production of
 CC animal models
 XX
 XX Sequence 93 AA;
 Query Match 100.0%; Score 504; DB 3; Length 93;
 Best Local Similarity 100.0%; Pred. No. 1e-52;
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MKISVAIIPFLLITLITGKTSSSRGPYPHPSGCCFTYTYKIPRORIMDYETNSQCS 60
 Db 1 MKISVAIIPFLLITLITGKTSSSRGPYPHPSGCCFTYTYKIPRORIMDYETNSQCS 60
 Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93
 Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93
 RESULT 8
 AAB68294
 ID AAB68294 standard; peptide; 93 AA.
 XX
 XX AAB68294;
 XX
 XX 09-JUL-2001 (first entry)
 XX
 XX Amino acid sequence of a fragment of the chemokine PHC-1.
 DE
 XX Chemokine; PHC-1; chemokine receptor; CCR-5 receptor; inflammation;
 KW cancer; restenosis; atherosclerosis; allergy; psoriasis; sarcoidosis;
 KW chronic contact dermatitis; inflammatory bowel disease; stroke;

KW multiple sclerosis; organ transplant rejection; infection; wound healing;
 KW bone healing; pain; diabetes; obesity; anorexia; bulimia; osteoporosis;
 KW Parkinson's disease; acute heart failure; hypotension; hypertension;
 KW urinary retention; angina pectoris; myocardial infarction; ischemia;
 KW ulcer; migraine; vomiting; psychotic disorder; neurological disorder;
 KW anxiety; schizophrenia; depression; delirium; dementia; dyskinesia;
 KW mental retardation; degenerative disease; neurodegenerative disease;
 KW Alzheimer's disease; Huntington's disease;
 KW Gilles de la Tourette's syndrome.
 XX
 XX Synthetic.
 XX
 XX WO200131016-A2.
 XX
 XX 03-MAY-2001.
 XX
 XX 25-OCT-2000; 2000WO-BE000128.
 XX
 XX 25-OCT-1999; 99DE-01051336.
 XX
 XX 22-JUN-2000; 2000EP-00870140.
 XX
 XX (EURO-) EUROSREEN SA.
 XX (KIRC/) KIRCHHOFF F.
 XX (FORS/) FORSSMANN W.
 XX
 XX Forssmann W, Detheux M, Parmentier M, Staendker L;
 XX WPI: 2001-308647/32.
 XX
 XX New processed human chemokines or their derivatives useful for preventing
 PT and treating viral infections, inflammation, cancer, atherosclerosis,
 PT multiple sclerosis, stroke, sarcoidosis or organ transplant rejection.
 XX
 XX Disclosure; Page 2; 50pp; English.
 XX
 XX The present sequence represents a fragment of an untruncated human
 CC chemokine PHC-1. Peptides derived from truncated PHC-1 are inhibitors of
 CC chemokine receptors, especially the CCR-5 receptor. Processed PHC-1
 CC chemokines are useful for prevention and treatment of a disease induced
 CC by viral infections, a bacterial agent or a protozoa. They are also
 CC useful for prevention and/or the treatment of a disease such as
 CC inflammation, cancers, restenosis, atherosclerosis, allergies, psoriasis,
 CC chronic contact dermatitis, inflammatory bowel disease, multiple
 CC sclerosis, stroke, sarcoidosis, organ transplant rejection, or infection
 CC induced by pathogenic agent. They are also useful for wound and bone
 CC healing, for treating pain, diabetes, obesity, anorexia, bulimia,
 CC Parkinson's disease, acute heart failure, hypotension, hypertension,
 CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,
 CC ischemia, ulcers, migraine, vomiting, psychotic and neurological
 CC disorders, including anxiety, schizophrenia, depression, delirium,
 CC dementia and severe mental retardation, degenerative diseases,
 CC neurodegenerative diseases such as Alzheimer's disease, and dyskinesias
 CC such as Huntington's disease or Gilles de la Tourette's syndrome
 XX
 XX Sequence 93 AA;
 Query Match 100.0%; Score 504; DB 4; Length 93;
 Best Local Similarity 100.0%; Pred. No. 1e-52;
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MKISVAIIPFLLITLITGKTSSSRGPYPHPSGCCFTYTYKIPRORIMDYETNSQCS 60
 Db 1 MKISVAIIPFLLITLITGKTSSSRGPYPHPSGCCFTYTYKIPRORIMDYETNSQCS 60
 Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93
 Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93
 RESULT 9
 AAB50992
 ID AAB50992 standard; protein; 93 AA.
 XX

```
AC AAB50992;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human PRO877 protein.
XX
KW Human; PRO; cardiac; antiangiogenic; antiarteriosclerotic; hypotensive;
KW vasotrophic; antiarheumatic; antiarthritic; antiinflammatory; cytostatic;
KW vulnerary; antianginal; gene therapy; cardiovascular disease;
KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;
KW wound healing.
XX
XX Homo sapiens.
XX
XX WO200073445-A2.
XX
XX 07-DEC-2000.
XX
XX 17-MAY-2000; 2000WO-US013705.
XX
XX 02-JUN-1999; 99WO-US012252.
XX 23-JUN-1999; 99US-0141037P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 28-JUL-1999; 99US-0146222P.
XX 01-SEP-1999; 99WO-US020111.
XX 30-NOV-1999; 99WO-US028313.
XX 30-NOV-1999; 99WO-US028409.
XX 02-DEC-1999; 99WO-US028565.
XX 16-DEC-1999; 99WO-US030095.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 24-FEB-2000; 2000WO-US005004.
XX 02-MAR-2000; 2000WO-US005841.
XX 10-MAR-2000; 2000WO-US006319.
XX 15-MAR-2000; 2000WO-US006884.
XX 21-MAR-2000; 2000WO-US007532.
XX 30-MAR-2000; 2000WO-US008439.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;
XX Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;
XX Pooni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
XX
XX WPI; 2001-025251/03.
XX N-PSDB; AAC90576.
XX
XX Seventeen nucleic acids encoding PRO polypeptides which are useful in
XX diagnosis and treatment of cardiovascular, endothelial or angiogenic
XX disorders in a mammal.
XX
XX Claim 71; Fig 28; 182pp; English.
XX
XX The present sequence is one of seventeen novel PRO polypeptides. The PRO
XX nucleic acids, polypeptides, agonists and antagonists are useful for
XX treating cardiovascular, endothelial or angiogenic disorders in a mammal.
XX Examples of these disorders include cardiac hypertrophy, trauma, cancer,
XX age-related macular degeneration, atherosclerosis, hypertension, arterial
XX stenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial
XX infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and
XX antagonists are also used to prevent tumour angiogenesis and for treating
XX periodontal diseases. They are also used to stimulate wound healing and
XX tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO
XX antibodies are useful for diagnosing a cardiovascular, endothelial or
XX angiogenic disorder
XX
XX Sequence 93 AA;
SQ
Query Match 100.0%; Score 504; DB 4; Length 93;

Best Local Similarity 100.0%; Pred. No. 1e-52; Indels 0; Gaps 0;
Matches 93; Conservative 0; Mismatches 0;

Qy 1 MKISVAAIPFELLITIALGTKESSRGYPHPSECCFTYTYKIQRIMDYVETNSQCS 60
Db 1 MKISVAAIPFELLITIALGTKESSRGYPHPSECCFTYTYKIQRIMDYVETNSQCS 60
Qy 61 KPGIVITIKRGHSVCTNPSPDKWQDYIKDMKEN 93
Db 61 KPGIVITIKRGHSVCTNPSPDKWQDYIKDMKEN 93

RESULT 10
ABB90773
ID ABB90773 standard; protein; 93 AA.
XX
XX ABB90773;
XX
XX 30-MAY-2002 (first entry)
XX
XX Human Tumour Endothelial Marker polypeptide SEQ ID NO 279.
XX
XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
XX normal endothelial marker; pan-endothelial marker; immunostimulant;
XX antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
XX polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
XX psoriasis.
XX
XX Homo sapiens.
XX
XX WO200210217-A2.
XX
XX 07-FEB-2002.
XX
XX 01-AUG-2001; 2001WO-US024031.
XX
XX 02-AUG-2000; 2000US-0222599P.
XX 11-AUG-2000; 2000US-0224360P.
XX 11-APR-2001; 2001US-0282850P.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX St Croix B, Kinzler KW, Vogelstein B;
XX
XX WPI; 2002-291856/33.
XX N-PSDB; ABL92128.
XX
XX An isolated molecule comprising an antibody variable region which
XX specifically binds to an extracellular domain of a tumor endothelial
XX marker (TEM) protein, useful for inhibiting tumor growth.
XX
XX Claim 59; Page 283; 331pp; English.
XX
XX The invention relates to an isolated molecule comprising an antibody
XX variable region which specifically binds to an extracellular domain of a
XX tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
XX ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
XX proteins have cytostatic, immunostimulant and antiangiogenic activity.
XX They are useful for inhibiting tumour growth, neoangiogenesis in subjects
XX bearing a vascularised tumour, polycystic kidney disease, diabetic
XX retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
XX genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
XX are disclosed, as are marker oligonucleotide sequences: tumour
XX endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
XX endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
XX (PEM) ABL91903-ABL91995
XX
XX Sequence 93 AA;
SQ
Query Match 100.0%; Score 504; DB 5; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-52; Indels 0; Gaps 0;
Matches 93; Conservative 0; Mismatches 0;
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Qy 1 MKISVAAPFLLITIALGKTESSRGYPHPSECCFTYTKIPRIMDYETNSQCS 60
Db 1 MKISVAAPFLLITIALGKTESSRGYPHPSECCFTYTKIPRIMDYETNSQCS 60

Qy 61 KPGIVFITKRGHVSCTNPSPDKWQDYIKDMKEN 93
Db 61 KPGIVFITKRGHVSCTNPSPDKWQDYIKDMKEN 93

RESULT 11
ABB90774
ID ABB90774 standard; protein; 93 AA.
XX
AC ABB90774;
XX
DT 30-MAY-2002 (first entry)
XX
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 281.
XX
KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW normal endothelial marker; pan-endothelial marker; immunostimulant;
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis.
XX
OS Homo sapiens.
XX
PN WO200210217-A2.
XX
PD 07-FEB-2002.
XX
PF 01-AUG-2001; 2001WO-US024031.
XX
PR 02-AUG-2000; 2000US-0222599P.
XX
PR 11-AUG-2000; 2000US-0224360P.
XX
PR 11-APR-2001; 2001US-0282850P.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI St Croix B, Kinzler KW, Vogelstein B;
XX
DR WPI; 2002-291856/33.
XX
DR N-PSDB; ABL92129.
XX
PT An isolated molecule comprising an antibody variable region which
PT specifically binds to an extracellular domain of a tumor endothelial
PT marker (TEM) protein, useful for inhibiting tumor growth.
XX
PS Disclosure; Page 284; 331pp; English.
XX
CC The invention relates to an isolated molecule comprising an antibody
CC variable region which specifically binds to an extracellular domain of a
CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects
CC bearing a vascularised tumour, polycystic kidney disease, diabetic
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
CC are disclosed, as are marker oligonucleotide sequences: tumour
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
CC (PEM) ABL91903-ABL91995
XX
SQ Sequence 93 AA;

Query Match 100.0%; Score 504; DB 5; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-52;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKISVAAPFLLITIALGKTESSRGYPHPSECCFTYTKIPRIMDYETNSQCS 60
Db 1 MKISVAAPFLLITIALGKTESSRGYPHPSECCFTYTKIPRIMDYETNSQCS 60

Qy 61 KPGIVFITKRGHVSCTNPSPDKWQDYIKDMKEN 93
Db 61 KPGIVFITKRGHVSCTNPSPDKWQDYIKDMKEN 93
```

```
Qy 61 KPGIVFITKRGHVSCTNPSPDKWQDYIKDMKEN 93
Db 61 KPGIVFITKRGHVSCTNPSPDKWQDYIKDMKEN 93

RESULT 12
ABB90772
ID ABB90772 standard; protein; 93 AA.
XX
AC ABB90772;
XX
DT 30-MAY-2002 (first entry)
XX
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 277.
XX
KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW normal endothelial marker; pan-endothelial marker; immunostimulant;
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis.
XX
OS Homo sapiens.
XX
PN WO200210217-A2.
XX
PD 07-FEB-2002.
XX
PF 01-AUG-2001; 2001WO-US024031.
XX
PR 02-AUG-2000; 2000US-0222599P.
XX
PR 11-AUG-2000; 2000US-0224360P.
XX
PR 11-APR-2001; 2001US-0282850P.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI St Croix B, Kinzler KW, Vogelstein B;
XX
DR WPI; 2002-291856/33.
XX
DR N-PSDB; ABL92127.
XX
PT An isolated molecule comprising an antibody variable region which
PT specifically binds to an extracellular domain of a tumor endothelial
PT marker (TEM) protein, useful for inhibiting tumor growth.
XX
PS Disclosure; Page 282; 331pp; English.
XX
CC The invention relates to an isolated molecule comprising an antibody
CC variable region which specifically binds to an extracellular domain of a
CC tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects
CC bearing a vascularised tumour, polycystic kidney disease, diabetic
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
CC are disclosed, as are marker oligonucleotide sequences: tumour
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
CC (PEM) ABL91903-ABL91995
XX
SQ Sequence 93 AA;

Query Match 100.0%; Score 504; DB 5; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-52;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKISVAAPFLLITIALGKTESSRGYPHPSECCFTYTKIPRIMDYETNSQCS 60
Db 1 MKISVAAPFLLITIALGKTESSRGYPHPSECCFTYTKIPRIMDYETNSQCS 60

Qy 61 KPGIVFITKRGHVSCTNPSPDKWQDYIKDMKEN 93
Db 61 KPGIVFITKRGHVSCTNPSPDKWQDYIKDMKEN 93
```

Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

RESULT 13

ABU61834

ID ABU61834 standard; protein; 93 AA.

XX AC ABU61834;

XX DT 15-AUG-2003 (first entry)

XX DE Chemokine HCC1.

XX KW Chemokine; HCC1; cell development; tissue culture development.

XX OS Primates.

XX PN US2003028005-A1.

XX PD 06-FEB-2003.

XX PF 11-AUG-1999; 99US-00372348.

XX PR 12-AUG-1998; 98US-0096328P.

XX PA (BAZA/) BAZAN J F.

XX PI Bazan JF;

XX DR WPI; 2003-466159/44.

XX DN New composition comprising HCC5, Dub11, Dub12, primate MD1 or MD2 or rodent MD2 polypeptide, useful for modulating physiology or development of a cell or tissue culture cells.

XX SQ Sequence 93 AA;

Query Match 100.0%; Score 504; DB 6; Length 93;

Best Local Similarity 100.0%; Pred. No. 1e-52;

Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKISVAAIPFFLLITIALGTKESSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60

Db 1 MKISVAAIPFFLLITIALGTKESSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60

Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

RESULT 14

ABU61832

ID ABU61832 standard; protein; 93 AA.

XX AC ABU61832;

XX DT 15-AUG-2003 (first entry)

XX DE Human MIP-4.

XX KW Human; MIP-4; cell development; tissue culture development.

XX OS Homo sapiens.

XX PN US2003028005-A1.

XX SQ Sequence 93 AA;

Query Match 100.0%; Score 504; DB 6; Length 93;

Best Local Similarity 100.0%; Pred. No. 1e-52;

Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKISVAAIPFFLLITIALGTKESSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60

Db 1 MKISVAAIPFFLLITIALGTKESSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60

Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

PD 06-FEB-2003.

XX 11-AUG-1999; 99US-00372348.

XX 12-AUG-1998; 98US-0096328P.

XX PA (BAZA/) BAZAN J F.

XX PI Bazan JF;

XX DR WPI; 2003-466159/44.

XX DN New composition comprising HCC5, Dub11, Dub12, primate MD1 or MD2 or rodent MD2 polypeptide, useful for modulating physiology or development of a cell or tissue culture cells.

XX FS Disclosure; Page 6-7; 77pp; English.

XX CC The invention relates to a novel chemokine, de-ubiquitination or cell surface protein. The composition is useful for modulating physiology or development of a cell or tissue culture cells. The present sequence represents the amino acid sequence of human MIP-4

XX SQ Sequence 93 AA;

Query Match 100.0%; Score 504; DB 6; Length 93;

Best Local Similarity 100.0%; Pred. No. 1e-52;

Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKISVAAIPFFLLITIALGTKESSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60

Db 1 MKISVAAIPFFLLITIALGTKESSSRGYPHPSECCFTYTYKIPRQIMDYETNSQCS 60

Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

RESULT 15

ABU61833

ID ABU61833 standard; protein; 93 AA.

XX AC ABU61833;

XX DT 15-AUG-2003 (first entry)

XX DE Pituitary expressed chemokine.

XX KW Pituitary expressed chemokine; chemokine; cell development; tissue culture development.

XX OS Primates.

XX PN US2003028005-A1.

XX PD 06-FEB-2003.

XX PF 11-AUG-1999; 99US-00372348.

XX PR 12-AUG-1998; 98US-0096328P.

XX PA (BAZA/) BAZAN J F.

XX PI Bazan JF;

XX DR WPI; 2003-466159/44.

XX DN New composition comprising HCC5, Dub11, Dub12, primate MD1 or MD2 or rodent MD2 polypeptide, useful for modulating physiology or development of a cell or tissue culture cells.

XX FS Disclosure; Page 6-7; 77pp; English.

XX PS

CC The invention relates to a novel chemokine, de-ubiquitination or cell
 CC surface protein. The composition is useful for modulating physiology or
 CC development of a cell or tissue culture cells. The present sequence
 CC represents the amino acid sequence of the pituitary expressed chemokine
 CC
 SQ Sequence 93 AA;

Query Match 100.0%; Score 504; DB 6; Length 93;
 Best Local Similarity 100.0%; Pred. No. 1e-52;
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKISVAALPFLITLITGKTSSSRGPHPSGCCFTYTYKIPRORIMDYETNSQCS 60
 Db 1 MKISVAALPFLITLITGKTSSSRGPHPSGCCFTYTYKIPRORIMDYETNSQCS 60
 Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93
 Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

RESULT 16
 ABUS4479
 ID ABUS4479 standard; protein; 93 AA.
 XX
 AC ABUS4479;
 XX
 DT 12-MAR-2003 (first entry)
 XX
 DE Human normal endothelial marker NEM 4.
 XX
 KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
 KW Tumour endothelial marker; normal endothelial marker; PEM;
 KW pan-endothelial marker; polycystic kidney disease; psoriasis;
 KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
 KW neovascularization; immune response; cytostatic; antidiabetic;
 KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200283874-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US008253.
 XX
 PR 11-APR-2001; 2001US-0282850P.
 PR 06-FEB-2002; 2002US-0354262P.
 XX
 PA (UWJO) UNIV JOHNS HOPKINS.
 XX
 PI Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
 XX
 PI WPI; 2003-093016/08.
 DR N-PSDB; ABX72052.
 DR
 XX New purified human transmembrane protein, designated as tumor endothelial
 PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
 PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
 PT psoriasis.
 XX
 PS Disclosure; Page 315; 374pp; English.
 XX
 CC The present invention relates to a novel method for the isolation of
 CC endothelial cells (ECs), and the identification of genes expressed in
 CC normal and tumour ECs. Tumour endothelial marker (TEM), normal
 CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
 CC identified in human ECs. The human EC marker proteins and the
 CC polynucleotide sequences encoding them are useful for detecting,
 CC diagnosing or treating tumours as well as polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
 CC useful for inhibiting neovascularization or tumour angiogenesis, for
 CC inducing an immune response to tumour endothelial cells in a patient, or
 CC for identifying candidate drugs for treating tumours. The present
 CC invention represents a human chemokine or NEM protein of the invention

CC sequence represents a human TEM or NEM protein of the invention
 XX
 SQ Sequence 93 AA;

Query Match 100.0%; Score 504; DB 6; Length 93;
 Best Local Similarity 100.0%; Pred. No. 1e-52;
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKISVAALPFLITLITGKTSSSRGPHPSGCCFTYTYKIPRORIMDYETNSQCS 60
 Db 1 MKISVAALPFLITLITGKTSSSRGPHPSGCCFTYTYKIPRORIMDYETNSQCS 60
 Qy 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93
 Db 61 KPGIVFITKRGHSVCTNPSPDKWQDYIKDMKEN 93

RESULT 17
 ABUS4481
 ID ABUS4481 standard; protein; 93 AA.
 XX
 AC ABUS4481;
 XX
 DT 12-MAR-2003 (first entry)
 XX
 DE Human normal endothelial marker NEM 17.
 XX
 KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
 KW Tumour endothelial marker; normal endothelial marker; PEM;
 KW pan-endothelial marker; polycystic kidney disease; psoriasis;
 KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
 KW neovascularization; immune response; cytostatic; antidiabetic;
 KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200283874-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US008253.
 XX
 PR 11-APR-2001; 2001US-0282850P.
 PR 06-FEB-2002; 2002US-0354262P.
 XX
 PA (UWJO) UNIV JOHNS HOPKINS.
 XX
 PI Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
 XX
 PI WPI; 2003-093016/08.
 DR N-PSDB; ABX72054.
 DR
 XX New purified human transmembrane protein, designated as tumor endothelial
 PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
 PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
 PT psoriasis.
 XX
 PS Disclosure; Page 317; 374pp; English.
 XX
 CC The present invention relates to a novel method for the isolation of
 CC endothelial cells (ECs), and the identification of genes expressed in
 CC normal and tumour ECs. Tumour endothelial marker (TEM), normal
 CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
 CC identified in human ECs. The human EC marker proteins and the
 CC polynucleotide sequences encoding them are useful for detecting,
 CC diagnosing or treating tumours as well as polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
 CC useful for inhibiting neovascularization or tumour angiogenesis, for
 CC inducing an immune response to tumour endothelial cells in a patient, or
 CC for identifying candidate drugs for treating tumours. The present
 CC invention represents a human TEM or NEM protein of the invention

XX Sequence 93 AA;
 SQ

Matches	93;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MKISVAAIPFLLITIALGFKTESSRGYPHPSECCFTYTYTKIPRORIMDYIETNSQCS	60						
Db	1	MKISVAAIPFLLITIALGFKTESSRGYPHPSECCFTYTYTKIPRORIMDYIETNSQCS	60						
Qy	61	KPGIVFITKRGHSVCTNPSPDKWQDYIKOMKEN	93						
Db	61	KPGIVFITKRGHSVCTNPSPDKWQDYIKOMKEN	93						
RESULT 19									
ABP76018									
ID	ABP76018 standard; protein; 93 AA.								
XX	AC ABP76018;								
XX	AC AC								
XX	DT 21-FEB-2003 (first entry)								
XX	DE Human GENSET protein SEQ ID 225.								
XX	XX								
KW	Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiac;								
KW	gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer;								
KW	inflammatory disease; immune disorder; neuromuscular; toxicity;								
KW	central nervous system; cardiovascular; gastrointestinal.								
XX	XX								
OS	Homo sapiens.								
XX	XX								
PN	WC200283898-A1.								
XX	XX								
PD	24-OCT-2002.								
XX	XX								
XX	18-APR-2001; 2001WO-IB000914.								
PF	XX								
XX	XX								
PR	18-APR-2001; 2001WO-IB000914.								
XX	XX								
PA	(GENSET) GENSET.								
XX	XX								
PI	Bejanin S, Tanaka H, Dumas Milne Edwards J, Jobert S, Giordano J;								
XX	XX								
DR	WPI; 2003-075548/07.								
XX	XX								
PT	New GENSET polynucleotides and polypeptides, useful for treating heavy								
PT	metal toxicity, cancer, inflammatory diseases, immune disorders, and the								
PT	neuromuscular, CNS, cardiovascular or gastrointestinal effects of the								
PT	toxicity.								
XX	XX								
PS	Claim 14; Page 426; 735pp; English.								
XX	XX								
CC	The present invention relates to novel GENSET polynucleotides (AB236404-								
CC	AB236911) encoding polypeptides (ABP75963-ABP76368). The polynucleotides								
CC	and polypeptides are useful in screening and diagnostic assays for								
CC	abnormal GENSET expression and/or biological activity. They are also								
CC	useful for screening of compounds for treating or preventing GENSET-								
CC	related disorders, such as heavy metal toxicity, cancer, inflammatory								
CC	diseases, immune disorders, and the neuromuscular, central nervous system								
CC	(CNS), cardiovascular or gastrointestinal effects of the toxicity								
XX	XX								
SQ	Sequence 93 AA;								
Query Match									
Best Local Similarity 100.0%; Score 504; DB 6; Length 93;									
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	MKISVAAIPFLLITIALGFKTESSRGYPHPSECCFTYTYTKIPRORIMDYIETNSQCS	60						
Db	1	MKISVAAIPFLLITIALGFKTESSRGYPHPSECCFTYTYTKIPRORIMDYIETNSQCS	60						
Qy	61	KPGIVFITKRGHSVCTNPSPDKWQDYIKOMKEN	93						
Db	61	KPGIVFITKRGHSVCTNPSPDKWQDYIKOMKEN	93						

RESULT 20

ADD06466
ID ADD06466 standard; protein; 93 AA.

AC ADD06466:

DT 01-JAN-2004 (first entry)

Human ckb1 protein SEQ ID NO:2.

human; chemokine beta1; Cxbl; anti-HIV; neuroprotective; antihypertensive; antiarthritic; antirheumatic; immunosuppressive; neurotrophic; antiinflammatory; antiasthmatic; anti-allergic; osteopathic; nephrotrophic; tuberculostatic; virucide; antiatherosclerotic; antimicrobial; infection; HIV; immune disorder; haematopoietic disorder; autoimmune disorder; multiple sclerosis; Grave's disease; arthritis; rheumatoid arthritis; transplant rejection; neurodegenerative disorder; Alzheimer's disease; inflammatory disease; asthma; allergic disorder; inflammatory bowel disease; osteoarthritis; colitis; inflammatory kidney disease; glomerulonephritis; infectious disease; tuberculosis; hepatitis infection; herpes viral infection; viral infection; proliferative disorder; atherosclerosis; human serum albumin; HSA.

OS Homo sapiens.

XX
PN
WO200297038-A2.

05-DEC-2002.

24-MAY-2002; 2002WO-US016525.

PR 25-MAY-2001; 2001US-0293212P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Bell A, Ruben SM;

WPI; 2003-140456/13.

DR N-PSDB; ADD06465.

Novel human chemokine beta1 protein comprising deletion in amino acids from amino and/or carboxy terminus, and is a fusion protein further comprising human serum albumin, is useful for treating multiple sclerosis, asthma.

Claim 1: SEQ ID NO 2: 423pp; English.

The present invention describes a human chemokine beta1 (Ckbl) protein (I) comprising a deletion in amino acid residues from the amino terminus and/or carboxy terminus of the 93 residue amino acid sequence (S1, see ADD064466). (I) has anti-HIV, neuroprotective, antithyroid, antiarthritic, antiasthmatic, immunosuppressive, nontropic, antiinflammatory, antiathermatic, antiallergic, osteopathic, nephrotrophic, tuberculostatic, virucide, antiatherosclerotic and antimicrobial activities. (I) is useful for preventing infection, preferably viral (human immunodeficiency virus (HIV)) infection, in a cell, by contacting the cell with (I). (I) is also useful for treating a disease, such as HIV infection or immune disorders, haematopoietic disorders, autoimmune disorders, multiple sclerosis, Grave's disease, arthritis, rheumatoid arthritis, transplant rejection, neurodegenerative disorders, Alzheimer's disease, inflammatory disease, asthma, allergic disorders, inflammatory bowel disease, osteoarthritis, colitis, inflammatory kidney diseases, glomerulonephritis, infectious disease, tuberculosis, hepatitis infections, herpes viral infection, viral infection, proliferative disorders or atherosclerosis, in an individual. (I) inhibits or abolishes the ability of HIV to bind to, enter into/fuse with (infect), and/or replicate in CR5 expressing cells. (I) also acts a CR5 agonists or antagonists, stimulate chemotaxis of CR5-expressing cells, inhibit CR5 ligand binding to a CR5 molecule, or upregulate or downregulate CR5 expression. (I) is useful as an immunological probe for the differential identification of the tissues or cell-types. (I)-human serum albumin (HSA) fusion proteins are useful for diagnosing, treating and preventing various disorders in mammals,

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DR WPI; 2003-598517/56.
DR N-PSDB; ADF15778.
XX
PT New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.
XX
PS Example 4; SEQ ID NO 511; 24pp; English.
XX
CC This invention relates to a novel albumin fusion protein having albumin
CC or biological activity. Human serum albumin is responsible for a
CC significant proportion of the osmotic pressure of serum and also
CC functions as a carrier of endogenous and exogenous ligands. The fusion of
CC albumin to a therapeutic protein may increase shelf-life and stability of
CC the therapeutic protein. The albumin fusion protein of the invention may
CC allow production of compositions with antidiabetic activity whilst the
CC nucleotide sequence which encodes it may be useful for gene therapy. The
CC albumin fusion protein is useful for preparing a composition for treating
CC diabetes mellitus. The present sequence is that of a therapeutic protein
CC which was fused with human albumin to create a novel albumin fusion
CC protein of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 93 AA;
Query Match 100.0%; Score 504; DB 7; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-52;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKISVAAIPFLLITLITGKTSSSRGYPHPSECCFTYTYKIPQRIMDYETNSQCS 60
Db 1 MKISVAAIPFLLITLITGKTSSSRGYPHPSECCFTYTYKIPQRIMDYETNSQCS 60
QY 61 KPGIVFITKRGHSHVCTNPSPDKWQDYIKDMKEN 93
Db 61 KPGIVFITKRGHSHVCTNPSPDKWQDYIKDMKEN 93
RESULT 22
ADFI6716
ID ADFI6716 standard; protein; 93 AA.
XX
AC ADFI6716;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human albumin fusion protein-related protein SeqID1818.
XX
KW albumin fusion protein; albumin activity; human serum albumin;
KW serum osmotic pressure; shelf-life; stability; antidiabetic;
KW gene therapy; diabetes mellitus; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003060071-A2.
XX
PD 24-JUL-2003.
XX
PF 23-DEC-2002; 2002WO-US040891.
XX
PR 21-DEC-2001; 2001US-0341811P.
PR 24-JAN-2002; 2002US-0350358P.
PR 28-JAN-2002; 2002US-0351360P.
PR 28-FEB-2002; 2002US-0359370P.
PR 28-FEB-2002; 2002US-0360000P.
PR 27-MAR-2002; 2002US-0367500P.
PR 08-APR-2002; 2002US-0370227P.
PR 10-MAY-2002; 2002US-0378950P.
PR 24-MAY-2002; 2002US-0382617P.
PR 28-MAY-2002; 2002US-0383123P.
PR 05-JUN-2002; 2002US-0385708P.
PR 10-JUL-2002; 2002US-0394625P.
PR 24-JUL-2002; 2002US-0398008P.
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PR 09-AUG-2002; 2002US-0402131P.
PR 13-AUG-2002; 2002US-0402708P.
PR 18-SEP-2002; 2002US-0411355P.
PR 18-SEP-2002; 2002US-0411426P.
PR 02-OCT-2002; 2002US-0414984P.
PR 11-OCT-2002; 2002US-0417611P.
PR 23-OCT-2002; 2002US-0420246P.
PR 05-NOV-2002; 2002US-0423623P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (DEL2 ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
XX
PI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
XX
XX WPI; 2003-598517/56.
DR N-PSDB; ADF16390.
XX
XX New albumin fusion protein, useful for preparing a composition for
XX treating diabetes mellitus.
PT
XX
PS Example 4; SEQ ID NO 1818; 24pp; English.
XX
CC This invention relates to a novel albumin fusion protein having albumin
CC or biological activity. Human serum albumin is responsible for a
CC significant proportion of the osmotic pressure of serum and also
CC functions as a carrier of endogenous and exogenous ligands. The fusion of
CC albumin to a therapeutic protein may increase shelf-life and stability of
CC the therapeutic protein. The albumin fusion protein of the invention may
CC allow production of compositions with antidiabetic activity whilst the
CC nucleotide sequence which encodes it may be useful for gene therapy. The
CC albumin fusion protein is useful for preparing a composition for treating
CC diabetes mellitus. The present sequence is that of a therapeutic protein
CC which was fused with human albumin to create a novel albumin fusion
CC protein of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 93 AA;
Query Match 100.0%; Score 504; DB 7; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-52;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKISVAAIPFLLITLITGKTSSSRGYPHPSECCFTYTYKIPQRIMDYETNSQCS 60
Db 1 MKISVAAIPFLLITLITGKTSSSRGYPHPSECCFTYTYKIPQRIMDYETNSQCS 60
QY 61 KPGIVFITKRGHSHVCTNPSPDKWQDYIKDMKEN 93
Db 61 KPGIVFITKRGHSHVCTNPSPDKWQDYIKDMKEN 93
RESULT 23
ADFI6713
ID ADFI6713 standard; protein; 93 AA.
XX
AC ADFI6713;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human albumin fusion protein-related protein SeqID1815.
XX
KW albumin fusion protein; albumin activity; human serum albumin;
KW serum osmotic pressure; shelf-life; stability; antidiabetic;
KW gene therapy; diabetes mellitus; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003060071-A2.
XX
PD 24-JUL-2003.
XX
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PF 23-DEC-2002; 2002WO-US040891.
XX
XX 21-DEC-2001; 2001US-0341811P.
PR 24-JAN-2002; 2002US-0350358P.
PR 28-JAN-2002; 2002US-0351360P.
PR 26-FEB-2002; 2002US-0359370P.
PR 28-FEB-2002; 2002US-0360000P.
PR 27-MAR-2002; 2002US-0367500P.
PR 08-APR-2002; 2002US-0370227P.
PR 10-MAY-2002; 2002US-0378950P.
PR 24-JUL-2002; 2002US-0394625P.
PR 09-AUG-2002; 2002US-0398008P.
PR 13-AUG-2002; 2002US-0402131P.
PR 18-SEP-2002; 2002US-0402708P.
PR 18-SEP-2002; 2002US-0411355P.
PR 02-OCT-2002; 2002US-0414984P.
PR 11-OCT-2002; 2002US-0417611P.
PR 23-OCT-2002; 2002US-0420246P.
PR 05-NOV-2002; 2002US-0423623P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
XX
PI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
XX WPI; 2003-598517/56.
DR N-PSDB; ADF16387.
XX
XX New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.
XX
XX Example 4; SEQ ID NO 1815; 24pp; English.
XX
XX This invention relates to a novel albumin fusion protein having albumin
CC or biological activity. Human serum albumin is responsible for a
CC significant proportion of the osmotic pressure of serum and also
CC functions as a carrier of endogenous and exogenous ligands. The fusion of
CC albumin to a therapeutic protein may increase shelf-life and stability of
CC the therapeutic protein. The albumin fusion protein of the invention may
CC allow production of compositions with antidiabetic activity whilst the
CC nucleotide sequence which encodes it may be useful for gene therapy. The
CC albumin fusion protein is useful for preparing a composition for treating
CC diabetes mellitus. The present sequence is that of a therapeutic protein
CC which was fused with human albumin to create a novel albumin fusion
CC protein of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
XX
XX Sequence 93 AA;
XX
XX Query Match 100.0%; Score 504; DB 7; Length 93;
XX Best Local Similarity 100.0%; Pred. No. 1e-52;
XX Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 MKISVAIPFLLITIALGTTESSSRGPHSPSCCTTYTKIPRQIMDYETNSQCS 60
Db 1 MKISVAIPFLLITIALGTTESSSRGPHSPSCCTTYTKIPRQIMDYETNSQCS 60
Qy 61 KPGIVFVTKRGHSVCTNPSPDKWQDYIKDMKEN 93
Db 61 KPGIVFVTKRGHSVCTNPSPDKWQDYIKDMKEN 93
XX
RESULT 24
ADF16715
ID ADF16715 standard; protein; 93 AA.
XX
AC ADF16715;
```

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XX 12-FEB-2004 (first entry)
XX
XX Human albumin fusion protein-related protein SeqID1817.
XX
XX albumin fusion protein; albumin activity; human serum albumin;
KW serum osmotic pressure; shelf-life; stability; antidiabetic;
KW gene therapy; diabetes mellitus; human; gene; ds.
XX
XX Homo sapiens.
XX
XX WO2003060071-A2.
XX
XX 24-JUL-2003.
XX
XX 23-DEC-2002; 2002WO-US040891.
XX
XX 21-DEC-2001; 2001US-0341811P.
PR 24-JAN-2002; 2002US-0350358P.
PR 28-JAN-2002; 2002US-0351360P.
PR 26-FEB-2002; 2002US-0359370P.
PR 28-FEB-2002; 2002US-0360000P.
PR 27-MAR-2002; 2002US-0367500P.
PR 08-APR-2002; 2002US-0370227P.
PR 10-MAY-2002; 2002US-0378950P.
PR 24-MAY-2002; 2002US-0382617P.
PR 28-MAY-2002; 2002US-0383123P.
PR 05-JUN-2002; 2002US-0385708P.
PR 10-JUL-2002; 2002US-0394625P.
PR 24-JUL-2002; 2002US-0398008P.
PR 09-AUG-2002; 2002US-0402131P.
PR 13-AUG-2002; 2002US-0402708P.
PR 18-SEP-2002; 2002US-0411355P.
PR 18-SEP-2002; 2002US-0414984P.
PR 02-OCT-2002; 2002US-0417611P.
PR 11-OCT-2002; 2002US-0420246P.
PR 23-OCT-2002; 2002US-0420246P.
PR 05-NOV-2002; 2002US-0423623P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
XX
PI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
XX WPI; 2003-598517/56.
DR N-PSDB; ADF16389.
XX
XX New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.
XX
XX Example 4; SEQ ID NO 1817; 24pp; English.
XX
XX This invention relates to a novel albumin fusion protein having albumin
CC or biological activity. Human serum albumin is responsible for a
CC significant proportion of the osmotic pressure of serum and also
CC functions as a carrier of endogenous and exogenous ligands. The fusion of
CC albumin to a therapeutic protein may increase shelf-life and stability of
CC the therapeutic protein. The albumin fusion protein of the invention may
CC allow production of compositions with antidiabetic activity whilst the
CC nucleotide sequence which encodes it may be useful for gene therapy. The
CC albumin fusion protein is useful for preparing a composition for treating
CC diabetes mellitus. The present sequence is that of a therapeutic protein
CC which was fused with human albumin to create a novel albumin fusion
CC protein of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
XX
XX Sequence 93 AA;
XX
XX Query Match 100.0%; Score 504; DB 7; Length 93;
XX Best Local Similarity 100.0%; Pred. No. 1e-52;
XX Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


QY 1 MKISVAAIPFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRORIMDYETNSQCS 60
 |||||
 DB 1 MKISVAAIPFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRORIMDYETNSQCS 60
 |||||
 QY 61 KPGIVFITRKGHSVCTNPSPDKWQDYIKDMKEN 93
 |||||
 DB 61 KPGIVFITRKGHSVCTNPSPDKWQDYIKDMKEN 93
 |||||

RESULT 25

ADFI5205
 ID ADFI5205 standard; protein; 93 AA.

XX AC ADFI5205;

DT 12-FEB-2004 (first entry)

XX Human albumin fusion protein-related protein SeqID503.

XX albumin fusion protein; albumin activity; human serum albumin;
 KW serum osmotic pressure; shelf-life; stability; antidiabetic;
 KW gene therapy; diabetes mellitus; human; gene; ds.

XX OS Homo sapiens.

XX PN WO2003060071-A2.

XX PD 24-JUL-2003.

XX PF 23-DEC-2002; 2002WO-US040891.

XX PR 21-DEC-2001; 2001US-0341811P.

PR 24-JAN-2002; 2002US-0350358P.

PR 28-JAN-2002; 2002US-0351360P.

PR 26-FEB-2002; 2002US-0359370P.

PR 28-FEB-2002; 2002US-0360000P.

PR 27-MAR-2002; 2002US-0367500P.

PR 08-APR-2002; 2002US-0370227P.

PR 10-MAY-2002; 2002US-0378950P.

PR 24-MAY-2002; 2002US-0382617P.

PR 28-MAY-2002; 2002US-0383123P.

PR 05-JUN-2002; 2002US-0385708P.

PR 10-JUL-2002; 2002US-0394625P.

PR 24-JUL-2002; 2002US-0398008P.

PR 09-AUG-2002; 2002US-0402131P.

PR 13-AUG-2002; 2002US-0402708P.

PR 18-SEP-2002; 2002US-0411355P.

PR 18-SEP-2002; 2002US-0411426P.

PR 02-OCT-2002; 2002US-0414984P.

PR 11-OCT-2002; 2002US-0417611P.

PR 23-OCT-2002; 2002US-0420246P.

PR 05-NOV-2002; 2002US-0423623P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (DELZ) DELTA BIOTECHNOLOGY LTD.

PA (PRIN-) PRINCIPIA PHARM CORP.

XX Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;

XX WPI; 2003-598517/56.

XX N-PSDB; ADFI5770.

XX New albumin fusion protein, useful for preparing a composition for
 PT treating diabetes mellitus.

PS Example 4; SEQ ID NO 503; 24pp; English.

XX This invention relates to a novel albumin fusion protein having albumin
 CC or biological activity. Human serum albumin is responsible for a
 CC significant proportion of the osmotic pressure of serum and also
 CC functions as a carrier of endogenous and exogenous ligands. The fusion of
 CC albumin to a therapeutic protein may increase shelf-life and stability of

CC the therapeutic protein. The albumin fusion protein of the invention may
 CC allow production of compositions with antidiabetic activity whilst the
 CC nucleotide sequence which encodes it may be useful for gene therapy. The
 CC albumin fusion protein is useful for preparing a composition for treating
 CC diabetes mellitus. The present sequence is that of a therapeutic protein
 CC which was fused with human albumin to create a novel albumin fusion
 CC protein of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences

XX Sequence 93 AA;

Query Match 100.0%; Score 504; DB 7; Length 93;

Best Local Similarity 100.0%; Pred. No. 1e-52;

Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKISVAAIPFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRORIMDYETNSQCS 60

|||||
 DB 1 MKISVAAIPFLLITIALGKTSSSRGYPHPSECCFTYTYKIPRORIMDYETNSQCS 60

QY 61 KPGIVFITRKGHSVCTNPSPDKWQDYIKDMKEN 93

|||||
 DB 61 KPGIVFITRKGHSVCTNPSPDKWQDYIKDMKEN 93

RESULT 26

ADFI5332

ID ADFI5332 standard; protein; 93 AA.

XX AC ADFI5332;

XX DT 12-FEB-2004 (first entry)

XX Human albumin fusion protein-related protein SeqID631.

XX albumin fusion protein; albumin activity; human serum albumin;
 KW serum osmotic pressure; shelf-life; stability; antidiabetic;
 KW gene therapy; diabetes mellitus; human; gene; ds.

XX OS Homo sapiens.

XX WO2003060071-A2.

XX PD 24-JUL-2003.

XX PF 23-DEC-2002; 2002WO-US040891.

XX PR 21-DEC-2001; 2001US-0341811P.

PR 24-JAN-2002; 2002US-0350358P.

PR 28-JAN-2002; 2002US-0351360P.

PR 26-FEB-2002; 2002US-0359370P.

PR 28-FEB-2002; 2002US-0360000P.

PR 27-MAR-2002; 2002US-0367500P.

PR 08-APR-2002; 2002US-0370227P.

PR 10-MAY-2002; 2002US-0378950P.

PR 24-MAY-2002; 2002US-0382617P.

PR 28-MAY-2002; 2002US-0383123P.

PR 05-JUN-2002; 2002US-0385708P.

PR 10-JUL-2002; 2002US-0394625P.

PR 24-JUL-2002; 2002US-0398008P.

PR 09-AUG-2002; 2002US-0402131P.

PR 13-AUG-2002; 2002US-0402708P.

PR 18-SEP-2002; 2002US-0411355P.

PR 18-SEP-2002; 2002US-0411426P.

PR 02-OCT-2002; 2002US-0414984P.

PR 11-OCT-2002; 2002US-0417611P.

PR 23-OCT-2002; 2002US-0420246P.

PR 05-NOV-2002; 2002US-0423623P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (DELZ) DELTA BIOTECHNOLOGY LTD.

PA (PRIN-) PRINCIPIA PHARM CORP.

XX


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PD 24-JUL-2003.
XX
XX 23-DEC-2002; 2002WO-US040891.
XX
XX 21-DEC-2001; 2001US-0341811P.
PR 24-JAN-2002; 2002US-0350358P.
PR 28-JAN-2002; 2002US-0351360P.
PR 26-FEB-2002; 2002US-0359370P.
PR 28-FEB-2002; 2002US-0360000P.
PR 27-MAR-2002; 2002US-0367500P.
PR 08-APR-2002; 2002US-0370227P.
PR 10-MAY-2002; 2002US-0378950P.
PR 24-MAY-2002; 2002US-0382617P.
PR 05-JUN-2002; 2002US-0398008P.
PR 09-AUG-2002; 2002US-0402708P.
PR 13-AUG-2002; 2002US-0411355P.
PR 18-SEP-2002; 2002US-0411426P.
PR 02-OCT-2002; 2002US-0414984P.
PR 11-OCT-2002; 2002US-0417611P.
PR 23-OCT-2002; 2002US-0420246P.
PR 05-NOV-2002; 2002US-0423623P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
XX
XX Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
XX
XX WPI; 2003-598517/56.
XX N-PSDB; ADF16388.
XX
XX New albumin fusion protein, useful for preparing a composition for
XX treating diabetes mellitus.
XX
XX Example 4; SEQ ID NO 1816; 24pp; English.
XX
XX This invention relates to a novel albumin fusion protein having albumin
XX or biological activity. Human serum albumin is responsible for a
XX significant proportion of the osmotic pressure of serum and also
XX functions as a carrier of endogenous and exogenous ligands. The fusion of
XX albumin to a therapeutic protein may increase shelf-life and stability of
XX the therapeutic protein. The albumin fusion protein of the invention may
XX allow production of compositions with antidiabetic activity whilst the
XX nucleotide sequence which encodes it may be useful for gene therapy. The
XX albumin fusion protein is useful for preparing a composition for treating
XX diabetes mellitus. The present sequence is that of a therapeutic protein
XX which was fused with human albumin to create a novel albumin fusion
XX protein of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification, but was obtained in electronic
XX format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
XX
XX Sequence 93 AA;
XX
XX Query Match 100.0%; Score 504; DB 7; Length 93;
XX Best Local Similarity 100.0%; Pred. No. 1e-52;
XX Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 MKISVAIPFLLITIALGKTESSSRGPHSPCCFTYTKIPRIMDYETNSQCS 60
Db 1 MKISVAIPFLLITIALGKTESSSRGPHSPCCFTYTKIPRIMDYETNSQCS 60
Qy 61 KPGIVFTIKRGHSVCTNPDKWQDYIKDMKEN 93
Db 61 KPGIVFTIKRGHSVCTNPDKWQDYIKDMKEN 93
XX
RESULT 29
ADF16739
ID ADF16739 standard; protein; 93 AA.
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XX
XX ADF16739;
XX
XX 12-FEB-2004 (first entry)
XX
XX Human albumin fusion protein-related protein SeqID1841.
XX
XX albumin fusion protein; albumin activity; human serum albumin;
XX serum osmotic pressure; shelf-life; stability; antidiabetic;
XX gene therapy; diabetes mellitus; human; gene; ds.
XX
XX Homo sapiens.
XX
XX WO2003060071-A2.
XX
XX 24-JUL-2003.
XX
XX 23-DEC-2002; 2002WO-US040891.
XX
XX 21-DEC-2001; 2001US-0341811P.
PR 24-JAN-2002; 2002US-0350358P.
PR 28-JAN-2002; 2002US-0351360P.
PR 26-FEB-2002; 2002US-0359370P.
PR 28-FEB-2002; 2002US-0360000P.
PR 27-MAR-2002; 2002US-0367500P.
PR 08-APR-2002; 2002US-0370227P.
PR 10-MAY-2002; 2002US-0378950P.
PR 24-MAY-2002; 2002US-0382617P.
PR 05-JUN-2002; 2002US-0385708P.
PR 10-JUL-2002; 2002US-0394625P.
PR 24-JUL-2002; 2002US-0398008P.
PR 09-AUG-2002; 2002US-0402131P.
PR 13-AUG-2002; 2002US-0402708P.
PR 18-SEP-2002; 2002US-0411355P.
PR 18-SEP-2002; 2002US-0411426P.
PR 02-OCT-2002; 2002US-0414984P.
PR 11-OCT-2002; 2002US-0417611P.
PR 23-OCT-2002; 2002US-0420246P.
PR 05-NOV-2002; 2002US-0423623P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
XX
XX Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
XX
XX WPI; 2003-598517/56.
XX N-PSDB; ADF16413.
XX
XX New albumin fusion protein, useful for preparing a composition for
XX treating diabetes mellitus.
XX
XX Example 4; SEQ ID NO 1841; 24pp; English.
XX
XX This invention relates to a novel albumin fusion protein having albumin
XX or biological activity. Human serum albumin is responsible for a
XX significant proportion of the osmotic pressure of serum and also
XX functions as a carrier of endogenous and exogenous ligands. The fusion of
XX albumin to a therapeutic protein may increase shelf-life and stability of
XX the therapeutic protein. The albumin fusion protein of the invention may
XX allow production of compositions with antidiabetic activity whilst the
XX nucleotide sequence which encodes it may be useful for gene therapy. The
XX albumin fusion protein is useful for preparing a composition for treating
XX diabetes mellitus. The present sequence is that of a therapeutic protein
XX which was fused with human albumin to create a novel albumin fusion
XX protein of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification, but was obtained in electronic
XX format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
XX
XX Sequence 93 AA;
XX
XX Query Match 100.0%; Score 504; DB 7; Length 93;
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Best Local Similarity 100.0%; Pred. No. 1e-52; Mismatches 0; Indels 0; Gaps 0;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKISVAAIPFFLLITIALGTTKTESSSRGPHSPCCFTYTYTKIPRQRMIDYETNSQCS 60
DB 1 MKISVAAIPFFLLITIALGTTKTESSSRGPHSPCCFTYTYTKIPRQRMIDYETNSQCS 60
QY 61 KPGIVFITKRGHSVCTNPNSDKWQDYIKDMKEN 93
DB 61 KPGIVFITKRGHSVCTNPNSDKWQDYIKDMKEN 93

RESULT 30
ADF15204
ID ADF15204 standard; protein; 93 AA.
XX
AC ADF15204;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human albumin fusion protein-related protein SeqID502.
XX
KW albumin fusion protein; albumin activity; human serum albumin;
KW serum osmotic pressure; shelf-life; stability; antidiabetic;
KW gene therapy; diabetes mellitus; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003060071-A2.
XX
PD 24-JUL-2003.
XX
PF 23-DEC-2002; 2002WO-US040891.
XX
PR 21-DEC-2001; 2001US-0341811P.
PR 24-JAN-2002; 2002US-0350358P.
PR 28-JAN-2002; 2002US-0351360P.
PR 26-FEB-2002; 2002US-0359370P.
PR 28-FEB-2002; 2002US-0360000P.
PR 27-MAR-2002; 2002US-0367500P.
PR 08-APR-2002; 2002US-0370227P.
PR 10-MAY-2002; 2002US-0378950P.
PR 24-MAY-2002; 2002US-0382617P.
PR 28-MAY-2002; 2002US-0383123P.
PR 05-JUN-2002; 2002US-0385708P.
PR 10-JUL-2002; 2002US-0394625P.
PR 24-JUL-2002; 2002US-0398008P.
PR 09-AUG-2002; 2002US-0402131P.
PR 13-AUG-2002; 2002US-0402708P.
PR 18-SEP-2002; 2002US-0411355P.
PR 18-SEP-2002; 2002US-0411426P.
PR 02-OCT-2002; 2002US-0414984P.
PR 11-OCT-2002; 2002US-0417611P.
PR 23-OCT-2002; 2002US-0420246P.
PR 05-NOV-2002; 2002US-0423623P.
XX
(HUMA-) HUMAN GENOME SCI INC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
XX
PI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
XX
DR WPI; 2003-598517/56.
DR N-PSDB; ADF15769.
XX
PT New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.
XX
PS Example 4; SEQ ID NO 502; 24pp; English.
XX
CC This invention relates to a novel albumin fusion protein having albumin
CC or biological activity. Human serum albumin is responsible for a
CC significant proportion of the osmotic pressure of serum and also

functions as a carrier of endogenous and exogenous ligands. The fusion of
albumin to a therapeutic protein may increase shelf-life and stability of
the therapeutic protein. The albumin fusion protein of the invention may
allow production of compositions with antidiabetic activity whilst the
nucleotide sequence which encodes it may be useful for gene therapy. The
albumin fusion protein is useful for preparing a composition for treating
diabetes mellitus. The present sequence is that of a therapeutic protein
which was fused with human albumin to create a novel albumin fusion
protein of the invention. Note: The sequence data for this patent did not
form part of the printed specification, but was obtained in electronic
format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences
XX Sequence 93 AA;
SQ

Query Match 100.0%; Score 504; DB 7; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-52;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKISVAAIPFFLLITIALGTTKTESSSRGPHSPCCFTYTYTKIPRQRMIDYETNSQCS 60
DB 1 MKISVAAIPFFLLITIALGTTKTESSSRGPHSPCCFTYTYTKIPRQRMIDYETNSQCS 60
QY 61 KPGIVFITKRGHSVCTNPNSDKWQDYIKDMKEN 93
DB 61 KPGIVFITKRGHSVCTNPNSDKWQDYIKDMKEN 93

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Job time : 166 secs

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